

# SEQUENCE LISTING

## (1) GENERAL INFORMATION:

### (i) APPLICANT:

- (A) NAME: Jens Koßmann
- (B) STREET ADDRESS: Golmer Fichten 9
- (C) CITY: Golm
- (E) COUNTRY: DE
- (F) POSTAL CODE: 14476

(ii) TITLE OF INVENTION: Plants synthesizing a modified starch, methods for their production as well as modified starch

(iii) NUMBER OF SEQUENCES: 4

### (iv) COMPUTER-READABLE VERSION:

- (A) DATA CARRIER: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

## (2) INFORMATION FOR SEQ ID NO: 1:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4856 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

### (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Solanum tuberosum
- (B) STRAIN: C.V. Berolina

### (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 105..4497

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CATCTTCATC GAATTCTTCG AAGCTTCTTC GCTAATTTC	60
GGTTTCTTC ACTCAAAATC	
GACGTTTCTA GCTGAACCTG AGTGAATTAA GCCAGTGGGA GGAT	116
ATG AGT AAT TCC	
Met Ser Asn Ser	
1	
TTA GGG AAT AAC TIG CTG TAC CAG GGA TTC CTA ACC TCA ACA GTG TIG	164
Leu Gly Asn Asn Leu Leu Tyr Gln Gly Phe Leu Thr Ser Thr Val Leu	
5 10 15 20	
GAA CAT AAA AGT AGA ATC AGT CCT CCT TGT GTT GGA GGC AAT TCT TTG	212
Glu His Lys Ser Arg Ile Ser Pro Pro Cys Val Gly Gly Asn Ser Leu	
25 30 35	

TTT CAA CAA CAA GTG ATC TCG AAA TCA CCT TTA TCA ACT GAG TTT CGA Phe Gln Gln Gln Val Ile Ser Lys Ser Pro Leu Ser Thr Glu Phe Arg 40 45 50	260
GGT AAC AGG TTA AAG GTG CAG AAA AAG AAA ATA CCT ATG GAA AAG AAG Gly Asn Arg Leu Lys Val Gln Lys Lys Lys Ile Pro Met Glu Lys Lys 55 60 65	308
CGT GCT TTT TCT AGT TCT CCT CAT GCT GTA CTT ACC ACT GAT ACC TCT Arg Ala Phe Ser Ser Ser Pro His Ala Val Leu Thr Thr Asp Thr Ser 70 75 80	356
TCT GAG CTA GCA GAA AAG TTC AGT CTA GGG GGG AAT ATT GAG CTA CAG Ser Glu Leu Ala Glu Lys Phe Ser Leu Gly Gly Asn Ile Glu Leu Gln 85 90 95 100	404
GTT GAT GTT AGG CCT CCC ACT TCA GGT GAT GTG TCC TTT GTG GAT TTT Val Asp Val Arg Pro Pro Thr Ser Gly Asp Val Ser Phe Val Asp Phe 105 110 115	452
CAA GTA ACA AAT GGT AGT GAT AAA CTG TTT TTG CAC TGG GGG GCA GTA Gln Val Thr Asn Gly Ser Asp Lys Leu Phe Leu His Trp Gly Ala Val 120 125 130	500
AAA TTC GGG AAA GAA ACA TGG TCT CTT CCG AAT GAT CGT CCA GAT GGG Lys Phe Gly Lys Glu Thr Trp Ser Leu Pro Asn Asp Arg Pro Asp Gly 135 140 145	548
ACC AAA GTG TAC AAG AAC AAA GCA CTT AGA ACT CCA TTT GTT AAA TCT Thr Lys Val Tyr Lys Asn Lys Ala Leu Arg Thr Pro Phe Val Lys Ser 150 155 160	596
GGC TCT AAC TCC ATC CTG AGA CTG GAG ATA CGA GAC ACT GCT ATC GAA Gly Ser Asn Ser Ile Leu Arg Leu Glu Ile Arg Asp Thr Ala Ile Glu 165 170 175 180	644
GCT ATT GAG TTT CTC ATA TAC GAT GAA GCC CAC GAT AAA TGG ATA AAG Ala Ile Glu Phe Leu Ile Tyr Asp Glu Ala His Asp Lys Trp Ile Lys 185 190 195	692
AAT AAT GGT GGT AAT TTT CGT GTC AAA TTG TCA AGA AAA GAG ATA CGA Asn Asn Gly Gly Asn Phe Arg Val Lys Leu Ser Arg Lys Glu Ile Arg 200 205 210	740
GGC CCA GAT GTT TCT GTT CCT GAG GAG CTT GTA CAG ATC CAA TCA TAT Gly Pro Asp Val Ser Val Pro Glu Glu Leu Val Gln Ile Gln Ser Tyr 215 220 225	788
TTG AGG TGG GAG AGG AAG GGA AAA CAG AAT TAC CCC CCT GAG AAA GAG Leu Arg Trp Glu Arg Lys Gly Lys Gln Asn Tyr Pro Pro Glu Lys Glu 230 235 240	836
AAG GAG GAA TAT GAG GCT GCT CGA ACT GTG CTA CAG GAG GAA ATA GCT Lys Glu Glu Tyr Glu Ala Ala Arg Thr Val Leu Gln Glu Glu Ile Ala 245 250 255 260	884
CGT GGT GCT TCC ATA CAG GAC ATT CGA GCA AGG CTA ACA AAA ACT AAT Arg Gly Ala Ser Ile Gln Asp Ile Arg Ala Arg Leu Thr Lys Thr Asn 265 270 275	932

GAT AAA AGT CAA AGC AAA GAA GAG CCT CTT CAT GTA ACA AAG AGT GAT Asp Lys Ser Gln Ser Lys Glu Glu Pro Leu His Val Thr Lys Ser Asp 280 285 290	980
ATA CCT GAT GAC CTT GCC CAA GCA CAA GCT TAC ATT AGG TGG GAG AAA Ile Pro Asp Asp Leu Ala Gln Ala Gln Ala Tyr Ile Arg Trp Glu Lys 295 300 305	1028
GCA GGA AAG CCG AAC TAT CCT CCA GAA AAG CAA ATT GAA GAA CTC GAA Ala Gly Lys Pro Asn Tyr Pro Pro Glu Lys Gln Ile Glu Glu Leu Glu 310 315 320	1076
GAA GCA AGA AGA GAA TTG CAA CTT GAG CTT GAG AAA GGC ATT ACC CTT Glu Ala Arg Arg Glu Leu Gln Leu Glu Leu Glu Lys Gly Ile Thr Leu 325 330 335 340	1124
GAT GAG TTG CGG AAA ACG ATT ACA AAA GGG GAG ATA AAA ACT AAG GTG Asp Glu Leu Arg Lys Thr Ile Thr Lys Gly Glu Ile Lys Thr Lys Val 345 350 355	1172
GAA AAG CAC CTG AAA AGA AGT TCT TTT GCC GTT GAA AGA ATC CAA AGA Glu Lys His Leu Lys Arg Ser Ser Phe Ala Val Glu Arg Ile Gln Arg 360 365 370	1220
AAG AAG AGA GAC TTT GGG CAT CTT ATT AAT AAG TAT ACT TCC AGT CCT Lys Lys Arg Asp Phe Gly His Leu Ile Asn Lys Tyr Thr Ser Ser Pro 375 380 385	1268
GCA GTA CAA GTA CAA AAG GTC TTG GAA GAA CCA CCA GCC TTA TCT AAA Ala Val Gln Val Gln Lys Val Leu Glu Glu Pro Pro Ala Leu Ser Lys 390 395 400	1316
ATT AAG CTG TAT GCC AAG GAG AAG GAG GAG CAG ATT GAT GAT CCG ATC Ile Lys Leu Tyr Ala Lys Glu Lys Glu Glu Gln Ile Asp Asp Pro Ile 405 410 415 420	1364
CTA AAT AAA AAG ATC TTT AAG GTC GAT GAT GGG GAG CTA CTG GTA CTG Leu Asn Lys Lys Ile Phe Lys Val Asp Asp Gly Glu Leu Leu Val Leu 425 430 435	1412
GTA GCA AAG TCC TCT GGG AAG ACA AAA GTA CAT CTA GCT ACA GAT CTG Val Ala Lys Ser Ser Gly Lys Thr Lys Val His Leu Ala Thr Asp Leu 440 445 450	1460
AAT CAG CCA ATT ACT CTT CAC TGG GCA TTA TCC AAA AGT CCT GGA GAG Asn Gln Pro Ile Thr Leu His Trp Ala Leu Ser Lys Ser Pro Gly Glu 455 460 465	1508
TGG ATG GTA CCA CCT TCA AGC ATA TTG CCT CCT GGG TCA ATT ATT TTA Trp Met Val Pro Pro Ser Ser Ile Leu Pro Pro Gly Ser Ile Ile Leu 470 475 480	1556
GAC AAG GCT GCC GAA ACA CCT TTT TCA GCC AGT TCT TCT GAT GGT CTA Asp Lys Ala Ala Glu Thr Pro Phe Ser Ala Ser Ser Ser Asp Gly Leu 485 490 495 500	1604
ACT TCT AAG GTA CAA TCT TTG GAT ATA GTA ATT GAA GAT GGC AAT TTT Thr Ser Lys Val Gln Ser Leu Asp Ile Val Ile Glu Asp Gly Asn Phe 505 510 515	1652

GTG GGG ATG CCA TTT GTT CTT TTG TCT GGT GAA AAA TGG ATT AAG AAC Val Gly Met Pro Phe Val Leu Leu Ser Gly Glu Lys Trp Ile Lys Asn 520 525 530	1700
CAA GGG TCG GAT TTC TAT GTT GGC TTC AGT GCT GCA TCC AAA TTA GCA Gln Gly Ser Asp Phe Tyr Val Gly Phe Ser Ala Ala Ser Lys Leu Ala 535 540 545	1748
CTC AAG GCT GCT GGG GAT GGC AGT GGA ACT GCA AAG TCT TTA CTG GAT Leu Lys Ala Ala Gly Asp Gly Ser Gly Thr Ala Lys Ser Leu Leu Asp 550 555 560	1796
AAA ATA GCA GAT ATG GAA AGT GAG GCT CAG AAG TCA TTT ATG CAC CGG Lys Ile Ala Asp Met Glu Ser Glu Ala Gln Lys Ser Phe Met His Arg 565 570 575	1844
TTT AAT ATT GCA GCT GAC TTG ATA GAA GAT GCC ACT AGT GCT GGT GAA Phe Asn Ile Ala Ala Asp Leu Ile Glu Asp Ala Thr Ser Ala Gly Glu 585 590 595	1892
CTT GGT TTT GCT GGA ATT CTT GTA TGG ATG AGG TTC ATG GCT ACA AGG Leu Gly Phe Ala Gly Ile Leu Val Trp Met Arg Phe Met Ala Thr Arg 600 605 610	1940
CAA CTG ATA TGG AAC AAA AAC TAT AAC GTA AAA CCA CGT GAA ATA AGC Gln Leu Ile Trp Asn Lys Asn Tyr Asn Val Lys Pro Arg Glu Ile Ser 615 620 625	1988
AAG GCT CAG GAC AGA CTT ACA GAC TTG TTG CAG AAT GCT TTC ACC AGT Lys Ala Gln Asp Arg Leu Thr Asp Leu Leu Gln Asn Ala Phe Thr Ser 630 635 640	2036
CAC CCT CAG TAC CGT GAA ATT TTG CGG ATG ATT ATG TCA ACT GTT GGA His Pro Gln Tyr Arg Glu Ile Leu Arg Met Ile Met Ser Thr Val Gly 645 650 655 660	2084
CGT GGA GGT GAA GGG GAT GTA GGA CAG CGA ATT AGG GAT GAA ATT TTG Arg Gly Gly Glu Gly Asp Val Gly Gln Arg Ile Arg Asp Glu Ile Leu 665 670 675	2132
GTC ATC CAG AGG AAC AAT GAC TGC AAG GGT GGT ATG ATG CAA GAA TGG Val Ile Gln Arg Asn Asn Asp Cys Lys Gly Gly Met Met Gln Glu Trp 680 685 690	2180
CAT CAG AAA TTG CAT AAT AAT ACT AGT CCT GAT GAT GTT GTG ATC TGT His Gln Lys Leu His Asn Asn Thr Ser Pro Asp Asp Val Val Ile Cys 695 700 705	2228
CAG GCA TTA ATT GAC TAC ATC AAG AGT GAT TTT GAT CTT GGT GTT TAT Gln Ala Leu Ile Asp Tyr Ile Lys Ser Asp Phe Asp Leu Gly Val Tyr 710 715 720	2276
TGG AAA ACC CTG AAT GAG AAC GGA ATA ACA AAA GAG CGT CTT TTG AGT Trp Lys Thr Leu Asn Glu Asn Gly Ile Thr Lys Glu Arg Leu Leu Ser 725 730 735 740	2324
TAT GAC CGT GCT ATC CAT TCT GAA CCA AAT TTT AGA GGA GAT CAA AAG Tyr Asp Arg Ala Ile His Ser Glu Pro Asn Phe Arg Gly Asp Gln Lys 745 750 755	2372

GGT GGT CTT TTG CGT GAT TTA GGT CAC TAT ATG AGA ACA TTG AAG GCA Gly Gly Leu Leu Arg Asp Leu Gly His Tyr Met Arg Thr Leu Lys Ala 760 765 770	2420
GTT CAT TCA GGT GCA GAT CTT GAG TCT GCT ATT GCA AAC TGC ATG GGC Val His Ser Gly Ala Asp Leu Glu Ser Ala Ile Ala Asn Cys Met Gly 775 780 785	2468
TAC AAA ACT GAG GGA GAA GGC TTT ATG GTT GGA GTC CAG ATA AAT CCT Tyr Lys Thr Glu Gly Glu Gly Phe Met Val Gly Val Gln Ile Asn Pro 790 795 800	2516
GTA TCA GGC TTG CCA TCT GGC TTT CAG GAC CTC CTC CAT TTT GTC TTA Val Ser Gly Leu Pro Ser Gly Phe Gln Asp Leu Leu His Phe Val Leu 805 810 815 820	2564
GAC CAT GTG GAA GAT AAA AAT GTG GAA ACT CTT CTT GAG AGA TTG CTA Asp His Val Glu Asp Lys Asn Val Glu Thr Leu Leu Glu Arg Leu Leu 825 830 835	2612
GAG GCT CGT GAG GAG CTT AGG CCC TTG CTT CTC AAA CCA AAC AAC CGT Glu Ala Arg Glu Glu Leu Arg Pro Leu Leu Leu Lys Pro Asn Asn Arg 840 845 850	2660
CTA AAG GAT CTG CTG TTT TTG GAC ATA GCA CTT GAT TCT ACA GTT AGA Leu Lys Asp Leu Leu Phe Leu Asp Ile Ala Leu Asp Ser Thr Val Arg 855 860 865	2708
ACA GCA GTA GAA AGG GGA TAT GAA GAA TTG AAC AAC GCT AAT CCT GAG Thr Ala Val Glu Arg Gly Tyr Glu Glu Leu Asn Asn Ala Asn Pro Glu 870 875 880	2756
AAA ATC ATG TAC TTC ATC TCC CTC GTT CTT GAA AAT CTC GCA CTC TCT Lys Ile Met Tyr Phe Ile Ser Leu Val Leu Glu Asn Leu Ala Leu Ser 885 890 895 900	2804
GTG GAC GAT AAT GAA GAT CTT GTT TAT TGC TTG AAG GGA TGG AAT CAA Val Asp Asp Asn Glu Asp Leu Val Tyr Cys Leu Lys Gly Trp Asn Gln 905 910 915	2852
GCT CTT TCA ATG TCC AAT GGT GGG GAC AAC CAT TGG GCT TTA TTT GCA Ala Leu Ser Met Ser Asn Gly Gly Asp Asn His Trp Ala Leu Phe Ala 920 925 930	2900
AAA GCT GTG CTT GAC AGA ACC CGT CTT GCA CTT GCA AGC AAG GCA GAG Lys Ala Val Leu Asp Arg Thr Arg Leu Ala Leu Ala Ser Lys Ala Glu 935 940 945	2948
TGG TAC CAT CAC TTA TTG CAG CCA TCT GCC GAA TAT CTA GGA TCA ATA Trp Tyr His His Leu Leu Gln Pro Ser Ala Glu Tyr Leu Gly Ser Ile 950 955 960	2996
CTT GGG GTG GAC CAA TGG GCT TTG AAC ATA TTT ACT GAA GAA ATT ATA Leu Gly Val Asp Gln Trp Ala Leu Asn Ile Phe Thr Glu Glu Ile Ile 965 970 975 980	3044
CGT GCT GGA TCA GCA GCT TCA TTA TCC TCT CTT CTT AAT AGA CTC GAT Arg Ala Gly Ser Ala Ala Ser Leu Ser Ser Leu Leu Asn Arg Leu Asp 985 990 995	3092

CCC GTG CTT CGG AAA ACT GCA AAT CTA GGA AGT TGG CAG ATT ATC AGT Pro Val Leu Arg Lys Thr Ala Asn Leu Gly Ser Trp Gln Ile Ile Ser 1000 1005 1010	3140
CCA GTT GAA GCC GTT GGA TAT GTT GTC GTT GTG GAT GAG TTG CTT TCA Pro Val Glu Ala Val Gly Tyr Val Val Val Val Asp Glu Leu Leu Ser 1015 1020 1025	3188
GTT CAG AAT GAA ATC TAC GAG AAG CCC ACG ATC TTA GTA GCA AAA TCT Val Gln Asn Glu Ile Tyr Glu Lys Pro Thr Ile Leu Val Ala Lys Ser 1030 1035 1040	3236
GTT AAA GGA GAG GAG GAA ATT CCT GAT GGT GCT GTT GCC CTG ATA ACA Val Lys Gly Glu Glu Glu Ile Pro Asp Gly Ala Val Ala Leu Ile Thr 1045 1050 1055 1060	3284
CCA GAC ATG CCA GAT GTT CTT TCA CAT GTT TCT GTT CGA GCT AGA AAT Pro Asp Met Pro Asp Val Leu Ser His Val Ser Val Arg Ala Arg Asn 1065 1070 1075	3332
GGG AAG GTT TGC TTT GCT ACA TGC TTT GAT CCC AAT ATA TTG GCT GAC Gly Lys Val Cys Phe Ala Thr Cys Phe Asp Pro Asn Ile Leu Ala Asp 1080 1085 1090	3380
CTC CAA GCA AAG GAA GGA AGG ATT TTG CTC TTA AAG CCT ACA CCT TCA Leu Gln Ala Lys Glu Gly Arg Ile Leu Leu Leu Lys Pro Thr Pro Ser 1095 1100 1105	3428
GAC ATA ATC TAT AGT GAG GTG AAT GAG ATT GAG CTC CAA AGT TCA AGT Asp Ile Ile Tyr Ser Glu Val Asn Glu Ile Glu Leu Gln Ser Ser Ser 1110 1115 1120	3476
AAC TTG GTA GAA GCT GAA ACT TCA GCA ACA CTT AGA TTG GTG AAA AAG Asn Leu Val Glu Ala Glu Thr Ser Ala Thr Leu Arg Leu Val Lys Lys 1125 1130 1135 1140	3524
CAA TTT GGT GGT TGT TAC GCA ATA TCA GCA GAT GAA TTC ACA AGT GAA Gln Phe Gly Gly Cys Tyr Ala Ile Ser Ala Asp Glu Phe Thr Ser Glu 1145 1150 1155	3572
ATG GTT GGA GCT AAA TCA CGT AAT ATT GCA TAT CTG AAA GGA AAA GTG Met Val Gly Ala Lys Ser Arg Asn Ile Ala Tyr Leu Lys Gly Lys Val 1160 1165 1170	3620
CCT TCC TCG GTG GGA ATT CCT ACG TCA GTA GCT CTT CCA TTT GGA GTC Pro Ser Ser Val Gly Ile Pro Thr Ser Val Ala Leu Pro Phe Gly Val 1175 1180 1185	3668
TTT GAG AAA GTA CTT TCA GAC GAC ATA AAT CAG GGA GTG GCA AAA GAG Phe Glu Lys Val Leu Ser Asp Asp Ile Asn Gln Gly Val Ala Lys Glu 1190 1195 1200	3716
TTG CAA ATT CTG ATG AAA AAA CTA TCT GAA GGA GAC TTC AGC GCT CTT Leu Gln Ile Leu Met Lys Lys Leu Ser Glu Gly Asp Phe Ser Ala Leu 1205 1210 1215 1220	3764
GGT GAA ATT CGC ACA ACG GTT TTA GAT CTT TCA GCA CCA GCT CAA TTG Gly Glu Ile Arg Thr Thr Val Leu Asp Leu Ser Ala Pro Ala Gln Leu 1225 1230 1235	3812

GTC AAA GAG CTG AAG GAG AAG ATG CAG GGT TCT GGC ATG CCT TGG CCT Val Lys Glu Leu Lys Glu Lys Met Gln Gly Ser Gly Met Pro Trp Pro 1240 1245 1250	3860
GGT GAT GAA GGT CCA AAG CGG TGG GAA CAA GCA TGG ATG GCC ATA AAA Gly Asp Glu Gly Pro Lys Arg Trp Glu Gln Ala Trp Met Ala Ile Lys 1255 1260 1265	3908
AAG GTG TGG GCT TCA AAA TGG AAT GAG AGA GCA TAC TTC AGC ACA AGG Lys Val Trp Ala Ser Lys Trp Asn Glu Arg Ala Tyr Phe Ser Thr Arg 1270 1275 1280	3956
AAG GTG AAA CTG GAT CAT GAC TAT CTG TGC ATG GCT GTC CTT GTT CAA Lys Val Lys Leu Asp His Asp Tyr Leu Cys Met Ala Val Leu Val Gln 1285 1290 1295 1300	4004
GAA ATA ATA AAT GCT GAT TAT GCA TTT GTC ATT CAC ACA ACC AAC CCA Glu Ile Ile Asn Ala Asp Tyr Ala Phe Val Ile His Thr Thr Asn Pro 1305 1310 1315	4052
TCT TCC GGA GAC GAC TCA GAA ATA TAT GCC GAG GTG GTC AGG GGC CTT Ser Ser Gly Asp Asp Ser Glu Ile Tyr Ala Glu Val Val Arg Gly Leu 1320 1325 1330	4100
GGG GAA ACA CTT GTT GGA GCT TAT CCA GGA CGT GCT TTG AGT TTT ATC Gly Glu Thr Leu Val Gly Ala Tyr Pro Gly Arg Ala Leu Ser Phe Ile 1335 1340 1345	4148
TGC AAG AAA AAG GAT CTC AAC TCT CCT CAA GTG TTA GGT TAC CCA AGC Cys Lys Lys Lys Asp Leu Asn Ser Pro Gln Val Leu Gly Tyr Pro Ser 1350 1355 1360	4196
AAA CCG ATC GGC CTT TTC ATA AAA AGA TCT ATC ATC TTC CGA TCT GAT Lys Pro Ile Gly Leu Phe Ile Lys Arg Ser Ile Ile Phe Arg Ser Asp 1365 1370 1375 1380	4244
TCC AAT GGG GAA GAT TTG GAA GGT TAT GCC GGT GCT GGC CTC TAC GAC Ser Asn Gly Glu Asp Leu Glu Gly Tyr Ala Gly Ala Gly Leu Tyr Asp 1385 1390 1395	4292
AGT GTA CCA ATG GAT GAG GAG GAA AAA GTT GTA ATT GAT TAC TCT TCC Ser Val Pro Met Asp Glu Glu Glu Lys Val Val Ile Asp Tyr Ser Ser 1400 1405 1410	4340
GAC CCA TTG ATA ACT GAT GGT AAC TTC CGC CAG ACA ATC CTG TCC AAC Asp Pro Leu Ile Thr Asp Gly Asn Phe Arg Gln Thr Ile Leu Ser Asn 1415 1420 1425	4388
ATT GCT CGT GCT GGA CAT GCT ATC GAG GAG CTA TAT GGC TCT CCT CAA Ile Ala Arg Ala Gly His Ala Ile Glu Glu Leu Tyr Gly Ser Pro Gln 1430 1435 1440	4436
GAC ATT GAG GGT GTA GTG AGG GAT GGA AAG ATT TAT GTC GTT CAG ACA Asp Ile Glu Gly Val Val Arg Asp Gly Lys Ile Tyr Val Val Gln Thr 1445 1450 1455 1460	4484
AGA CCA CAG ATG T GATTATATTC TCGTTGTATG TTGTTCCAGAG AAGACCACAG Arg Pro Gln Met	4537

ATGTGATCAT ATTCTCATTG TATCAGATCT GTGACCACTT ACCTGATACC TCCCATGAAG 4597  
 TTACCTGTAT GATTATACGT GATCCAAAGC CATCACATCA TGTTACCTTT CAGCTATTGG 4657  
 AGGAGAAGTG AGAAGTAGGA ATTGCAATAT GAGGAATAAT AAGAAAAACT TTGTAAAAGC 4717  
 TAAATTAGCT GGGTATGATA TAGGGAGAAA TGTTGTAACA TTGTACTATA TATAGTATAT 4777  
 ACACACGCAT TATGTATTGC ATTATGCACT GAATAATATC GCAGCATCAA AGAAGAAATC 4837  
 CTTTGGGTGG TTTCAAAAA 4856

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1464 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ser Asn Ser Leu Gly Asn Asn Leu Tyr Gln Gly Phe Leu Thr  
 1 5 10 15  
 Ser Thr Val Leu Glu His Lys Ser Arg Ile Ser Pro Pro Cys Val Gly  
 20 25 30  
 Gly Asn Ser Leu Phe Gln Gln Gln Val Ile Ser Lys Ser Pro Leu Ser  
 35 40 45  
 Thr Glu Phe Arg Gly Asn Arg Leu Lys Val Gln Lys Lys Ile Pro  
 50 55 60  
 Met Glu Lys Lys Arg Ala Phe Ser Ser Ser Pro His Ala Val Leu Thr  
 65 70 75 80  
 Thr Asp Thr Ser Ser Glu Leu Ala Glu Lys Phe Ser Leu Gly Gly Asn  
 85 90 95  
 Ile Glu Leu Gln Val Asp Val Arg Pro Pro Thr Ser Gly Asp Val Ser  
 100 105 110  
 Phe Val Asp Phe Gln Val Thr Asn Gly Ser Asp Lys Leu Phe Leu His  
 115 120 125  
 Trp Gly Ala Val Lys Phe Gly Lys Glu Thr Trp Ser Leu Pro Asn Asp  
 130 135 140  
 Arg Pro Asp Gly Thr Lys Val Tyr Lys Asn Lys Ala Leu Arg Thr Pro  
 145 150 155 160  
 Phe Val Lys Ser Gly Ser Asn Ser Ile Leu Arg Leu Glu Ile Arg Asp  
 165 170 175  
 Thr Ala Ile Glu Ala Ile Glu Phe Leu Ile Tyr Asp Glu Ala His Asp  
 180 185 190



Lys Trp Ile Lys Asn Asn Gly Gly Asn Phe Arg Val Lys Leu Ser Arg  
 195 200 205  
 Lys Glu Ile Arg Gly Pro Asp Val Ser Val Pro Glu Glu Leu Val Gln  
 210 215 220  
 Ile Gln Ser Tyr Leu Arg Trp Glu Arg Lys Gly Lys Gln Asn Tyr Pro  
 225 230 235 240  
 Pro Glu Lys Glu Lys Glu Glu Tyr Glu Ala Ala Arg Thr Val Leu Gln  
 245 250 255  
 Glu Glu Ile Ala Arg Gly Ala Ser Ile Gln Asp Ile Arg Ala Arg Leu  
 260 265 270  
 Thr Lys Thr Asn Asp Lys Ser Gln Ser Lys Glu Glu Pro Leu His Val  
 275 280 285  
 Thr Lys Ser Asp Ile Pro Asp Asp Leu Ala Gln Ala Gln Ala Tyr Ile  
 290 295 300  
 Arg Trp Glu Lys Ala Gly Lys Pro Asn Tyr Pro Pro Glu Lys Gln Ile  
 305 310 315 320  
 Glu Glu Leu Glu Glu Ala Arg Arg Glu Leu Gln Leu Glu Leu Glu Lys  
 325 330 335  
 Gly Ile Thr Leu Asp Glu Leu Arg Lys Thr Ile Thr Lys Gly Glu Ile  
 340 345 350  
 Lys Thr Lys Val Glu Lys His Leu Lys Arg Ser Ser Phe Ala Val Glu  
 355 360 365  
 Arg Ile Gln Arg Lys Lys Arg Asp Phe Gly His Leu Ile Asn Lys Tyr  
 370 375 380  
 Thr Ser Ser Pro Ala Val Gln Val Gln Lys Val Leu Glu Glu Pro Pro  
 385 390 395 400  
 Ala Leu Ser Lys Ile Lys Leu Tyr Ala Lys Glu Lys Glu Glu Gln Ile  
 405 410 415  
 Asp Asp Pro Ile Leu Asn Lys Lys Ile Phe Lys Val Asp Asp Gly Glu  
 420 425 430  
 Leu Leu Val Leu Val Ala Lys Ser Ser Gly Lys Thr Lys Val His Leu  
 435 440 445  
 Ala Thr Asp Leu Asn Gln Pro Ile Thr Leu His Trp Ala Leu Ser Lys  
 450 455 460  
 Ser Pro Gly Glu Trp Met Val Pro Pro Ser Ser Ile Leu Pro Pro Gly  
 465 470 475 480  
 Ser Ile Ile Leu Asp Lys Ala Ala Glu Thr Pro Phe Ser Ala Ser Ser  
 485 490 495  
 Ser Asp Gly Leu Thr Ser Lys Val Gln Ser Leu Asp Ile Val Ile Glu  
 500 505 510

Asp Gly Asn Phe Val Gly Met Pro Phe Val Leu Leu Ser Gly Glu Lys  
 515 520 525  
 Trp Ile Lys Asn Gln Gly Ser Asp Phe Tyr Val Gly Phe Ser Ala Ala  
 530 535 540  
 Ser Lys Leu Ala Leu Lys Ala Ala Gly Asp Gly Ser Gly Thr Ala Lys  
 545 550 555 560  
 Ser Leu Leu Asp Lys Ile Ala Asp Met Glu Ser Glu Ala Gln Lys Ser  
 565 570 575  
 Phe Met His Arg Phe Asn Ile Ala Ala Asp Leu Ile Glu Asp Ala Thr  
 580 585 590  
 Ser Ala Gly Glu Leu Gly Phe Ala Gly Ile Leu Val Trp Met Arg Phe  
 595 600 605  
 Met Ala Thr Arg Gln Leu Ile Trp Asn Lys Asn Tyr Asn Val Lys Pro  
 610 615 620  
 Arg Glu Ile Ser Lys Ala Gln Asp Arg Leu Thr Asp Leu Leu Gln Asn  
 625 630 635 640  
 Ala Phe Thr Ser His Pro Gln Tyr Arg Glu Ile Leu Arg Met Ile Met  
 645 650 655  
 Ser Thr Val Gly Arg Gly Gly Glu Gly Asp Val Gly Gln Arg Ile Arg  
 660 665 670  
 Asp Glu Ile Leu Val Ile Gln Arg Asn Asn Asp Cys Lys Gly Gly Met  
 675 680 685  
 Met Gln Glu Trp His Gln Lys Leu His Asn Asn Thr Ser Pro Asp Asp  
 690 695 700  
 Val Val Ile Cys Gln Ala Leu Ile Asp Tyr Ile Lys Ser Asp Phe Asp  
 705 710 715 720  
 Leu Gly Val Tyr Trp Lys Thr Leu Asn Glu Asn Gly Ile Thr Lys Glu  
 725 730 735  
 Arg Leu Leu Ser Tyr Asp Arg Ala Ile His Ser Glu Pro Asn Phe Arg  
 740 745 750  
 Gly Asp Gln Lys Gly Gly Leu Leu Arg Asp Leu Gly His Tyr Met Arg  
 755 760 765  
 Thr Leu Lys Ala Val His Ser Gly Ala Asp Leu Glu Ser Ala Ile Ala  
 770 775 780  
 Asn Cys Met Gly Tyr Lys Thr Glu Gly Glu Gly Phe Met Val Gly Val  
 785 790 795 800  
 Gln Ile Asn Pro Val Ser Gly Leu Pro Ser Gly Phe Gln Asp Leu Leu  
 805 810 815  
 His Phe Val Leu Asp His Val Glu Asp Lys Asn Val Glu Thr Leu Leu  
 820 825 830

Glu Arg Leu Leu Glu Ala Arg Glu Glu Leu Arg Pro Leu Leu Leu Lys  
 835 840 845  
 Pro Asn Asn Arg Leu Lys Asp Leu Leu Phe Leu Asp Ile Ala Leu Asp  
 850 855 860  
 Ser Thr Val Arg Thr Ala Val Glu Arg Gly Tyr Glu Glu Leu Asn Asn  
 865 870 875 880  
 Ala Asn Pro Glu Lys Ile Met Tyr Phe Ile Ser Leu Val Leu Glu Asn  
 885 890 895  
 Leu Ala Leu Ser Val Asp Asp Asn Glu Asp Leu Val Tyr Cys Leu Lys  
 900 905 910  
 Gly Trp Asn Gln Ala Leu Ser Met Ser Asn Gly Gly Asp Asn His Trp  
 915 920 925  
 Ala Leu Phe Ala Lys Ala Val Leu Asp Arg Thr Arg Leu Ala Leu Ala  
 930 935 940  
 Ser Lys Ala Glu Trp Tyr His His Leu Leu Gln Pro Ser Ala Glu Tyr  
 945 950 955 960  
 Leu Gly Ser Ile Leu Gly Val Asp Gln Trp Ala Leu Asn Ile Phe Thr  
 965 970 975  
 Glu Glu Ile Ile Arg Ala Gly Ser Ala Ala Ser Leu Ser Ser Leu Leu  
 980 985 990  
 Asn Arg Leu Asp Pro Val Leu Arg Lys Thr Ala Asn Leu Gly Ser Trp  
 995 1000 1005  
 Gln Ile Ile Ser Pro Val Glu Ala Val Gly Tyr Val Val Val Val Asp  
 1010 1015 1020  
 Glu Leu Leu Ser Val Gln Asn Glu Ile Tyr Glu Lys Pro Thr Ile Leu  
 1025 1030 1035 1040  
 Val Ala Lys Ser Val Lys Gly Glu Glu Glu Ile Pro Asp Gly Ala Val  
 1045 1050 1055  
 Ala Leu Ile Thr Pro Asp Met Pro Asp Val Leu Ser His Val Ser Val  
 1060 1065 1070  
 Arg Ala Arg Asn Gly Lys Val Cys Phe Ala Thr Cys Phe Asp Pro Asn  
 1075 1080 1085  
 Ile Leu Ala Asp Leu Gln Ala Lys Glu Gly Arg Ile Leu Leu Leu Lys  
 1090 1095 1100  
 Pro Thr Pro Ser Asp Ile Ile Tyr Ser Glu Val Asn Glu Ile Glu Leu  
 1105 1110 1115 1120  
 Gln Ser Ser Ser Asn Leu Val Glu Ala Glu Thr Ser Ala Thr Leu Arg  
 1125 1130 1135  
 Leu Val Lys Lys Gln Phe Gly Gly Cys Tyr Ala Ile Ser Ala Asp Glu  
 1140 1145 1150

Phe Thr Ser Glu Met Val Gly Ala Lys Ser Arg Asn Ile Ala Tyr Leu  
 1155 1160 1165  
 Lys Gly Lys Val Pro Ser Ser Val Gly Ile Pro Thr Ser Val Ala Leu  
 1170 1175 1180  
 Pro Phe Gly Val Phe Glu Lys Val Leu Ser Asp Asp Ile Asn Gln Gly  
 1185 1190 1195 1200  
 Val Ala Lys Glu Leu Gln Ile Leu Met Lys Lys Leu Ser Glu Gly Asp  
 1205 1210 1215  
 Phe Ser Ala Leu Gly Glu Ile Arg Thr Thr Val Leu Asp Leu Ser Ala  
 1220 1225 1230  
 Pro Ala Gln Leu Val Lys Glu Leu Lys Glu Lys Met Gln Gly Ser Gly  
 1235 1240 1245  
 Met Pro Trp Pro Gly Asp Glu Gly Pro Lys Arg Trp Glu Gln Ala Trp  
 1250 1255 1260  
 Met Ala Ile Lys Lys Val Trp Ala Ser Lys Trp Asn Glu Arg Ala Tyr  
 1265 1270 1275 1280  
 Phe Ser Thr Arg Lys Val Lys Leu Asp His Asp Tyr Leu Cys Met Ala  
 1285 1290 1295  
 Val Leu Val Gln Glu Ile Ile Asn Ala Asp Tyr Ala Phe Val Ile His  
 1300 1305 1310  
 Thr Thr Asn Pro Ser Ser Gly Asp Asp Ser Glu Ile Tyr Ala Glu Val  
 1315 1320 1325  
 Val Arg Gly Leu Gly Glu Thr Leu Val Gly Ala Tyr Pro Gly Arg Ala  
 1330 1335 1340  
 Leu Ser Phe Ile Cys Lys Lys Lys Asp Leu Asn Ser Pro Gln Val Leu  
 1345 1350 1355 1360  
 Gly Tyr Pro Ser Lys Pro Ile Gly Leu Phe Ile Lys Arg Ser Ile Ile  
 1365 1370 1375  
 Phe Arg Ser Asp Ser Asn Gly Glu Asp Leu Glu Gly Tyr Ala Gly Ala  
 1380 1385 1390  
 Gly Leu Tyr Asp Ser Val Pro Met Asp Glu Glu Glu Lys Val Val Ile  
 1395 1400 1405  
 Asp Tyr Ser Ser Asp Pro Leu Ile Thr Asp Gly Asn Phe Arg Gln Thr  
 1410 1415 1420  
 Ile Leu Ser Asn Ile Ala Arg Ala Gly His Ala Ile Glu Glu Leu Tyr  
 1425 1430 1435 1440  
 Gly Ser Pro Gln Asp Ile Glu Gly Val Val Arg Asp Gly Lys Ile Tyr  
 1445 1450 1455  
 Val Val Gln Thr Arg Pro Gln Met  
 1460

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1918 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Solanum tuberosum*
- (B) STRAIN: C.V. Desiree

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..1555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCA GAG TGG TAC CAT CAC TTA TTG CAG CCA TCT GCC GAA TAT CTA GGA	48
Ala Glu Trp Tyr His His Leu Leu Gln Pro Ser Ala Glu Tyr Leu Gly	
1 5 10 15	
TCA ATA CTT GGG GTG GAC CAA TGG GCT TTG AAC ATA TTT ACT GAA GAA	96
Ser Ile Leu Gly Val Asp Gln Trp Ala Leu Asn Ile Phe Thr Glu Glu	
20 25 30	
ATT ATA CGT GCT GGA TCA GCA GCT TCA TTA TCC TCT CTT CTT AAT AGA	144
Ile Ile Arg Ala Gly Ser Ala Ala Ser Leu Ser Ser Leu Leu Asn Arg	
35 40 45	
CTC GAT CCC GTG CTT CGG AAA ACT GCA AAT CTA GGA AGT TGG CAG ATT	192
Leu Asp Pro Val Leu Arg Lys Thr Ala Asn Leu Gly Ser Trp Gln Ile	
50 55 60	
ATC AGT CCA GTT GAA GCC GTT GGA TAT GTT GTC GTT GTG GAT GAG TTG	240
Ile Ser Pro Val Glu Ala Val Gly Tyr Val Val Val Val Asp Glu Leu	
65 70 75 80	
CTT TCA GTT CAG AAT GAA ATC TAC GAG AAG CCC ACG ATC TTA GTA GCA	288
Leu Ser Val Gln Asn Glu Ile Tyr Glu Lys Pro Thr Ile Leu Val Ala	
85 90 95	
AAA TCT GTT AAA GGA GAG GAG GAA ATT CCT GAT GGT GCT GTT GCC CTG	336
Lys Ser Val Lys Gly Glu Glu Glu Ile Pro Asp Gly Ala Val Ala Leu	
100 105 110	
ATA ACA CCA GAC ATG CCA GAT GTT CTT TCA CAT GTT TCT GTT CGA GCT	384
Ile Thr Pro Asp Met Pro Asp Val Leu Ser His Val Ser Val Arg Ala	
115 120 125	
AGA AAT GGG AAG GTT TGC TTT GCT ACA TGC TTT GAT CCC AAT ATA TTG	432
Arg Asn Gly Lys Val Cys Phe Ala Thr Cys Phe Asp Pro Asn Ile Leu	
130 135 140	
GCT GAC CTC CAA GCA AAG GAA GGA AGG ATT TTG CTC TTA AAG CCT ACA	480
Ala Asp Leu Gln Ala Lys Glu Gly Arg Ile Leu Leu Leu Lys Pro Thr	
145 150 155 160	

CCT TCA GAC ATA ATC TAT AGT GAG GTG AAT GAG ATT GAG CTC CAA AGT Pro Ser Asp Ile Ile Tyr Ser Glu Val Asn Glu Ile Glu Leu Gln Ser 165 170 175	528
TCA AGT AAC TTG GTA GAA GCT GAA ACT TCA GCA ACA CTT AGA TTG GTG Ser Ser Asn Leu Val Glu Ala Glu Thr Ser Ala Thr Leu Arg Leu Val 180 185 190	576
AAA AAG CAA TTT GGT GGT TGT TAC GCA ATA TCA GCA GAT GAA TTC ACA Lys Lys Gln Phe Gly Gly Cys Tyr Ala Ile Ser Ala Asp Glu Phe Thr 195 200 205	624
AGT GAA ATG GTT GGA GCT AAA TCA CGT AAT ATT GCA TAT CTG AAA GGA Ser Glu Met Val Gly Ala Lys Ser Arg Asn Ile Ala Tyr Leu Lys Gly 210 215 220	672
AAA GTG CCT TCC TCG GTG GGA ATT CCT ACG TCA GTA GCT CTT CCA TTT Lys Val Pro Ser Ser Val Gly Ile Pro Thr Ser Val Ala Leu Pro Phe 225 230 235 240	720
GGA GTC TTT GAG AAA GTA CTT TCA GAC GAC ATA AAT CAG GGA GTG GCA Gly Val Phe Glu Lys Val Leu Ser Asp Asp Ile Asn Gln Gly Val Ala 245 250 255	768
AAA GAG TTG CAA ATT CTG ACA AAA AAA CTA TCT GAA GGA GAC TTT AGC Lys Glu Leu Gln Ile Leu Thr Lys Lys Leu Ser Glu Gly Asp Phe Ser 260 265 270	816
GCT CTT GGT GAA ATT CGC ACA ACG GTT TTA GAT CTT TCG ACA CCA GCT Ala Leu Gly Glu Ile Arg Thr Thr Val Leu Asp Leu Ser Thr Pro Ala 275 280 285	864
CAA TTG GTC AAA GAG CTG AAG GAG AAG ATG CAG GGT TCT GGC ATG CCT Gln Leu Val Lys Glu Leu Lys Glu Lys Met Gln Gly Ser Gly Met Pro 290 295 300	912
TGG CCT GGT GAT GAA GGT CCA AAG CGG TGG GAA CAA GCA TGG ATG GCC Trp Pro Gly Asp Glu Gly Pro Lys Arg Trp Glu Gln Ala Trp Met Ala 305 310 315 320	960
ATA AAA AAG GTG TGG GCT TCA AAA TGG AAT GAG AGA GCA TAC TTC AGC Ile Lys Lys Val Trp Ala Ser Lys Trp Asn Glu Arg Ala Tyr Phe Ser 325 330 335	1008
ACA AGG AAG GTG AAA CTG GAT CAT GAC TAT CTG TGC ATG GCT GTC CTT Thr Arg Lys Val Lys Leu Asp His Asp Tyr Leu Cys Met Ala Val Leu 340 345 350	1056
GTT CAA GAA ATA ATA AAT GCT GAT TAT GCA TTT GTC ATT CAC ACA ACC Val Gln Glu Ile Ile Asn Ala Asp Tyr Ala Phe Val Ile His Thr Thr 355 360 365	1104
AAC CCA TCT TCC GGA GAC GAC TCA GAA ATA TAT GCC GAG GTG GTC AGG Asn Pro Ser Ser Gly Asp Asp Ser Glu Ile Tyr Ala Glu Val Val Arg 370 375 380	1152
GGC CTT GGG GAA ACA CTT GTT GGA GCT TAT CCA GGA CGT GCT TTG AGT Gly Leu Gly Glu Thr Leu Val Gly Ala Tyr Pro Gly Arg Ala Leu Ser 385 390 395 400	1200

TTT ATC TGC AAG AAA AAG GAT CTC AAC TCT CCT CAA GTG TTA GGT TAC Phe Ile Cys Lys Lys Lys Asp Leu Asn Ser Pro Gln Val Leu Gly Tyr 405 410 415	1248
CCA AGC AAA CCG ATC GGC CTT TTC ATA AAA AGA TCT ATC TTC CGA Pro Ser Lys Pro Ile Gly Leu Phe Ile Lys Arg Ser Ile Ile Phe Arg 420 425 430	1296
TCT GAT TCC AAT GGG GAA GAT TTG GAA GGT TAT GCC GGT GCT GGC CTC Ser Asp Ser Asn Gly Glu Asp Leu Glu Gly Tyr Ala Gly Ala Gly Leu 435 440 445	1344
TAC GAC AGT GTA CCA ATG GAT GAG GAG GAA AAA GTT GTA ATT GAT TAC Tyr Asp Ser Val Pro Met Asp Glu Glu Glu Lys Val Val Ile Asp Tyr 450 455 460	1392
TCT TCC GAC CCA TTG ATA ACT GAT GGT AAC TTC CGC CAG ACA ATC CTG Ser Ser Asp Pro Leu Ile Thr Asp Gly Asn Phe Arg Gln Thr Ile Leu 465 470 475 480	1440
TCC AAC ATT GCT CGT GCT GGA CAT GCT ATC GAG GAG CTA TAT GGC TCT Ser Asn Ile Ala Arg Ala Gly His Ala Ile Glu Glu Leu Tyr Gly Ser 485 490 495	1488
CCT CAA GAC ATT GAG GGT GTA GTG AGG GAT GGA AAG ATT TAT GTC GTT Pro Gln Asp Ile Glu Gly Val Val Arg Asp Gly Lys Ile Tyr Val Val 500 505 510	1536
CAG ACA AGA CCA CAG ATG T GATTATATTC TCGTTGTATG TTGTTACAG Gln Thr Arg Pro Gln Met 515	1585
AAGACCACAG ATGTGATCAT ATTCTCATTG TATCAGATCT GTGACCACTT ACCTGATACC	1645
TCCCATGAAG TTACCTGTAT GATTATACGT GATCCAAAGC CATCACATCA TGTTACACCTT	1705
CAGCTATTGG AGGAGAAGTG AGAAGTAGGA ATTGCAATAT GAGGAATAAT AAGAAAAACT	1765
TTGTAAAGC TAAATTAGCT GGGTATGATA TAGGGAGAAA TGTGTAACAA TTGTACTATA	1825
TATAGTATAT ACACACGCAT TATGTATTGC ATTATGCACT GAATAATATC GCAGCATCAA	1885
AGAAGAAATC CTTTGGGTGG TTTCAAAAAA AAA	1918

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Ala Glu Trp Tyr His His Leu Leu Gln Pro Ser Ala Glu Tyr Leu Gly 1 5 10 15
Ser Ile Leu Gly Val Asp Gln Trp Ala Leu Asn Ile Phe Thr Glu Glu 20 25 30

Ile Ile Arg Ala Gly Ser Ala Ala Ser Leu Ser Ser Leu Leu Asn Arg  
 35 40 45  
 Leu Asp Pro Val Leu Arg Lys Thr Ala Asn Leu Gly Ser Trp Gln Ile  
 50 55 60  
 Ile Ser Pro Val Glu Ala Val Gly Tyr Val Val Val Val Asp Glu Leu  
 65 70 75 80  
 Leu Ser Val Gln Asn Glu Ile Tyr Glu Lys Pro Thr Ile Leu Val Ala  
 85 90 95  
 Lys Ser Val Lys Gly Glu Glu Glu Ile Pro Asp Gly Ala Val Ala Leu  
 100 105 110  
 Ile Thr Pro Asp Met Pro Asp Val Leu Ser His Val Ser Val Arg Ala  
 115 120 125  
 Arg Asn Gly Lys Val Cys Phe Ala Thr Cys Phe Asp Pro Asn Ile Leu  
 130 135 140  
 Ala Asp Leu Gln Ala Lys Glu Gly Arg Ile Leu Leu Leu Lys Pro Thr  
 145 150 155 160  
 Pro Ser Asp Ile Ile Tyr Ser Glu Val Asn Glu Ile Glu Leu Gln Ser  
 165 170 175  
 Ser Ser Asn Leu Val Glu Ala Glu Thr Ser Ala Thr Leu Arg Leu Val  
 180 185 190  
 Lys Lys Gln Phe Gly Gly Cys Tyr Ala Ile Ser Ala Asp Glu Phe Thr  
 195 200 205  
 Ser Glu Met Val Gly Ala Lys Ser Arg Asn Ile Ala Tyr Leu Lys Gly  
 210 215 220  
 Lys Val Pro Ser Ser Val Gly Ile Pro Thr Ser Val Ala Leu Pro Phe  
 225 230 235 240  
 Gly Val Phe Glu Lys Val Leu Ser Asp Asp Ile Asn Gln Gly Val Ala  
 245 250 255  
 Lys Glu Leu Gln Ile Leu Thr Lys Lys Leu Ser Glu Gly Asp Phe Ser  
 260 265 270  
 Ala Leu Gly Glu Ile Arg Thr Thr Val Leu Asp Leu Ser Thr Pro Ala  
 275 280 285  
 Gln Leu Val Lys Glu Leu Lys Glu Lys Met Gln Gly Ser Gly Met Pro  
 290 295 300  
 Trp Pro Gly Asp Glu Gly Pro Lys Arg Trp Glu Gln Ala Trp Met Ala  
 305 310 315 320  
 Ile Lys Lys Val Trp Ala Ser Lys Trp Asn Glu Arg Ala Tyr Phe Ser  
 325 330 335  
 Thr Arg Lys Val Lys Leu Asp His Asp Tyr Leu Cys Met Ala Val Leu  
 340 345 350



Val Gln Glu Ile Ile Asn Ala Asp Tyr Ala Phe Val Ile His Thr Thr  
 355 360 365  
 Asn Pro Ser Ser Gly Asp Asp Ser Glu Ile Tyr Ala Glu Val Val Arg  
 370 375 380  
 Gly Leu Gly Glu Thr Leu Val Gly Ala Tyr Pro Gly Arg Ala Leu Ser  
 385 390 395 400  
 Phe Ile Cys Lys Lys Lys Asp Leu Asn Ser Pro Gln Val Leu Gly Tyr  
 405 410 415  
 Pro Ser Lys Pro Ile Gly Leu Phe Ile Lys Arg Ser Ile Ile Phe Arg  
 420 425 430  
 Ser Asp Ser Asn Gly Glu Asp Leu Glu Gly Tyr Ala Gly Ala Gly Leu  
 435 440 445  
 Tyr Asp Ser Val Pro Met Asp Glu Glu Glu Lys Val Val Ile Asp Tyr  
 450 455 460  
 Ser Ser Asp Pro Leu Ile Thr Asp Gly Asn Phe Arg Gln Thr Ile Leu  
 465 470 475 480  
 Ser Asn Ile Ala Arg Ala Gly His Ala Ile Glu Glu Leu Tyr Gly Ser  
 485 490 495  
 Pro Gln Asp Ile Glu Gly Val Val Arg Asp Gly Lys Ile Tyr Val Val  
 500 505 510  
 Gln Thr Arg Pro Gln Met  
 515

# SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Jens Kossmann  
Ruth Lorberth
- (ii) TITLE OF INVENTION: PLANTS WHICH SYNTHESIZE A MODIFIED STARCH,  
PROCESS FOR THE PRODUCTION THEREOF AND MODIFIED STARCH
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: FISH & NEAVE
  - (B) STREET: 1251 Avenue of the Americas
  - (C) CITY: New York
  - (D) STATE: New York
  - (E) COUNTRY: USA
  - (F) ZIP: 10020
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) Classification:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: PCT/EP96/04109
  - (B) FILING DATE: 19-SEP-1996
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: DE 19547733.2
  - (B) FILING DATE: 20-DEC-1995
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: DE 19534759.5
  - (B) FILING DATE: 19-SEP-1995
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Haley Jr., James F.
  - (B) REGISTRATION NUMBER: 27,794
  - (C) REFERENCE/DOCKET NUMBER: GFB-5
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 212-596-9000
  - (B) TELEFAX: 212-596-9090

## (2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4856 base pairs
  - (B) TYPE: nucleotide
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Solanum tuberosum*  
(B) STRAIN: C.V. Berolina

## (ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 105..4497

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CATCTTCATC GAATTTCTCG AAGCTTCTTC GCTAATTTCC TGGTTTCTTC ACTCAAAATC	60
GACGTTTCTA GCTGAACCTTG AGTGAATTAA GCCAGTGGGA GGAT ATG AGT AAT TCC	116
Met Ser Asn Ser	
1	
TTA GGG AAT AAC TTG CTG TAC CAG GGA TTC CTA ACC TCA ACA GTG TTG	164
Leu Gly Asn Asn Leu Leu Tyr Gln Gly Phe Leu Thr Ser Thr Val Leu	
5 10 15 20	
GAA CAT AAA AGT AGA ATC AGT CCT CCT TGT GTT GGA GGC AAT TCT TTG	212
Glu His Lys Ser Arg Ile Ser Pro Pro Cys Val Gly Gly Asn Ser Leu	
25 30 35	
TTT CAA CAA CAA GTG ATC TCG AAA TCA CCT TTA TCA ACT GAG TTT CGA	260
Phe Gln Gln Gln Val Ile Ser Lys Ser Pro Leu Ser Thr Glu Phe Arg	
40 45 50	
GGT AAC AGG TTA AAG GTG CAG AAA AAG AAA ATA CCT ATG GAA AAG AAG	308
Gly Asn Arg Leu Lys Val Gln Lys Lys Ile Pro Met Glu Lys Lys	
55 60 65	
CGT GCT TTT TCT AGT TCT CCT CAT GCT GTA CTT ACC ACT GAT ACC TCT	356
Arg Ala Phe Ser Ser Ser Pro His Ala Val Leu Thr Thr Asp Thr Ser	
70 75 80	
TCT GAG CTA GCA GAA AAG TTC AGT CTA GGG GGG AAT ATT GAG CTA CAG	404
Ser Glu Leu Ala Glu Lys Phe Ser Leu Gly Gly Asn Ile Glu Leu Gln	
85 90 95 100	
GTT GAT GTT AGG CCT CCC ACT TCA GGT GAT GTG TCC TTT GTG GAT TTT	452
Val Asp Val Arg Pro Pro Thr Ser Gly Asp Val Ser Phe Val Asp Phe	
105 110 115	
CAA GTA ACA AAT GGT AGT GAT AAA CTG TTT TTG CAC TGG GGG GCA GTA	500
Gln Val Thr Asn Gly Ser Asp Lys Leu Phe Leu His Trp Gly Ala Val	
120 125 130	
AAA TTC GGG AAA GAA ACA TGG TCT CTT CCG AAT GAT CGT CCA GAT GGG	548
Lys Phe Gly Lys Glu Thr Trp Ser Leu Pro Asn Asp Arg Pro Asp Gly	
135 140 145	
ACC AAA GTG TAC AAG AAC AAA GCA CTT AGA ACT CCA TTT GTT AAA TCT	596
Thr Lys Val Tyr Lys Asn Lys Ala Leu Arg Thr Pro Phe Val Lys Ser	
150 155 160	
GGC TCT AAC TCC ATC CTG AGA CTG GAG ATA CGA GAC ACT GCT ATC GAA	644
Gly Ser Asn Ser Ile Leu Arg Leu Glu Ile Arg Asp Thr Ala Ile Glu	
165 170 175 180	
GCT ATT GAG TTT CTC ATA TAC GAT GAA GCC CAC GAT AAA TGG ATA AAG	692
Ala Ile Glu Phe Leu Ile Tyr Asp Glu Ala His Asp Lys Trp Ile Lys	
185 190 195	

AAT AAT GGT GGT AAT TTT CGT GTC AAA TTG TCA AGA AAA GAG ATA CGA Asn Asn Gly Gly Asn Phe Arg Val Lys Leu Ser Arg Lys Glu Ile Arg 200 205 210	740
GGC CCA GAT GTT TCT GTT CCT GAG GAG CTT GTA CAG ATC CAA TCA TAT Gly Pro Asp Val Ser Val Pro Glu Glu Leu Val Gln Ile Gln Ser Tyr 215 220 225	788
TTG AGG TGG GAG AGG AAG GGA AAA CAG AAT TAC CCC CCT GAG AAA GAG Leu Arg Trp Glu Arg Lys Gly Lys Gln Asn Tyr Pro Pro Glu Lys Glu 230 235 240	836
AAG GAG GAA TAT GAG GCT GCT CGA ACT GTG CTA CAG GAG GAA ATA GCT Lys Glu Glu Tyr Glu Ala Ala Arg Thr Val Leu Gln Glu Glu Ile Ala 245 250 255	884
CGT GGT GCT TCC ATA CAG GAC ATT CGA GCA AGG CTA ACA AAA ACT AAT Arg Gly Ala Ser Ile Gln Asp Ile Arg Ala Arg Leu Thr Lys Thr Asn 265 270 275	932
GAT AAA AGT CAA AGC AAA GAA GAG CCT CTT CAT GTA ACA AAG AGT GAT Asp Lys Ser Gln Ser Lys Glu Glu Pro Leu His Val Thr Lys Ser Asp 280 285	980
ATA CCT GAT GAC CTT GCC CAA GCA CAA GCT TAC ATT AGG TGG GAG AAA Ile Pro Asp Asp Leu Ala Gln Ala Gln Ala Tyr Ile Arg Trp Glu Lys 295 300 305	1028
GCA GGA AAG CCG AAC TAT CCT CCA GAA AAG CAA ATT GAA GAA CTC GAA Ala Gly Lys Pro Asn Tyr Pro Pro Glu Lys Gln Ile Glu Glu Leu Glu 310 315 320	1076
GAA GCA AGA AGA GAA TTG CAA CTT GAG CTT GAG AAA GGC ATT ACC CTT Glu Ala Arg Arg Glu Leu Gln Leu Glu Leu Lys Gly Ile Thr Leu 325 330 335 340	1124
GAT GAG TTG CGG AAA ACG ATT ACA AAA GGG GAG ATA AAA ACT AAG GTG Asp Glu Leu Arg Lys Thr Ile Thr Lys Gly Glu Ile Lys Thr Lys Val 345 350 355	1172
GAA AAG CAC CTG AAA AGA AGT TCT TTT GCC GTT GAA AGA ATC CAA AGA Glu Lys His Leu Lys Arg Ser Ser Phe Ala Val Glu Arg Ile Gln Arg 360 365 370	1220
AAG AAG AGA GAC TTT GGG CAT CTT ATT AAT AAG TAT ACT TCC AGT CCT Lys Lys Arg Asp Phe Gly His Leu Ile Asn Lys Tyr Thr Ser Ser Pro 375 380 385	1268
GCA GTA CAA GTA CAA AAG GTC TTG GAA GAA CCA CCA GCC TTA TCT AAA Ala Val Gln Val Gln Lys Val Leu Glu Glu Pro Pro Ala Leu Ser Lys 390 395 400	1316
ATT AAG CTG TAT GCC AAG GAG AAG GAG GAG CAG ATT GAT GAT CCG ATC Ile Lys Leu Tyr Ala Lys Glu Lys Glu Glu Gln Ile Asp Asp Pro Ile 405 410 415 420	1364
CTA AAT AAA AAG ATC TTT AAG GTC GAT GAT GGG GAG CTA CTG GTA CTG Leu Asn Lys Lys Ile Phe Lys Val Asp Asp Gly Glu Leu Leu Val Leu 425 430 435	1412
GTA GCA AAG TCC TCT GGG AAG ACA AAA GTA CAT CTA GCT ACA GAT CTG Val Ala Lys Ser Ser Gly Lys Thr Lys Val His Leu Ala Thr Asp Leu 440 445 450	1460

AAT CAG CCA ATT ACT CTT CAC TGG GCA TTA TCC AAA AGT CCT GGA GAG Asn Gln Pro Ile Thr Leu His Trp Ala Leu Ser Lys Ser Pro Gly Glu 455 460 465	1508
TGG ATG GTA CCA CCT TCA AGC ATA TTG CCT CCT GGG TCA ATT ATT TTA Trp Met Val Pro Pro Ser Ser Ile Leu Pro Pro Gly Ser Ile Ile Leu 470 475 480	1556
GAC AAG GCT GCC GAA ACA CCT TTT TCA GCC AGT TCT TCT GAT GGT CTA Asp Lys Ala Ala Glu Thr Pro Phe Ser Ala Ser Ser Ser Asp Gly Leu 485 490 495 500	1604
ACT TCT AAG GTA CAA TCT TTG GAT ATA GTA ATT GAA GAT GGC AAT TTT Thr Ser Lys Val Gln Ser Leu Asp Ile Val Ile Glu Asp Gly Asn Phe 505 510 515	1652
GTG GGG ATG CCA TTT GTT CTT TTG TCT GGT GAA AAA TGG ATT AAG AAC Val Gly Met Pro Phe Val Leu Leu Ser Gly Glu Lys Trp Trp Lys Asn 520 525 530	1700
CAA GGG TCG GAT TTC TAT GTT GGC TTC AGT GCT GCA TCC AAA TTA GCA Gln Gly Ser Asp Phe Tyr Val Gly Phe Ser Ala Ala Ser Lys Leu Ala 535 540 545	1748
CTC AAG GCT GCT GGG GAT GGC AGT GGA ACT GCA AAG TCT TTA CTG GAT Leu Lys Ala Ala Gly Asp Gly Ser Gly Thr Ala Lys Ser Leu Leu Asp 550 555 560	1796
AAA ATA GCA GAT ATG GAA AGT GAG GCT CAG AAG TCA TTT ATG CAC CGG Lys Ile Ala Asp Met Glu Ser Glu Ala Gln Lys Ser Phe Met His Arg 565 570 575 580	1844
TTT AAT ATT GCA GCT GAC TTG ATA GAA GAT GCC ACT AGT GCT GGT GAA Phe Asn Ile Ala Ala Asp Leu Ile Glu Asp Ala Thr Ser Ala Gly Glu 585 590 595	1892
CTT GGT TTT GCT GGA ATT CTT GTA TGG ATG AGG TTC ATG GCT ACA AGG Leu Gly Phe Ala Gly Ile Leu Val Trp Met Arg Phe Met Ala Thr Arg 600 605 610	1940
CAA CTG ATA TGG AAC AAA AAC TAT AAC GTA AAA CCA CGT GAA ATA AGC Gln Leu Ile Trp Asn Lys Asn Tyr Asn Val Lys Pro Arg Glu Ile Ser 615 620 625	1988
AAG GCT CAG GAC AGA CTT ACA GAC TTG TTG CAG AAT GCT TTC ACC AGT Lys Ala Gln Asp Arg Leu Thr Asp Leu Leu Gln Asn Ala Phe Thr Ser 630 635 640	2036
CAC CCT CAG TAC CGT GAA ATT TTG CGG ATG ATT ATG TCA ACT GTT GGA His Pro Gln Tyr Arg Glu Ile Leu Arg Met Ile Met Ser Thr Val Gly 645 650 655 660	2084
CGT GGA GGT GAA GGG GAT GTA GGA CAG CGA ATT AGG GAT GAA ATT TTG Arg Gly Gly Glu Gly Asp Val Gly Gln Arg Ile Arg Asp Glu Ile Leu 665 670 675	2132
GTC ATC CAG AGG AAC AAT GAC TGC AAG GGT GGT ATG ATG CAA GAA TGG Val Ile Gln Arg Asn Asn Asp Cys Lys 685 680 690	2180
CAT CAG AAA TTG CAT AAT AAT ACT AGT CCT GAT GAT GTT GTG ATC TGT His Gln Lys Leu His Asn Asn Thr Ser Pro Asp Asp Val Val Ile Cys	2228

695	700	705	
CAG GCA TTA ATT GAC TAC ATC AAG AGT GAT TTT GAT CTT GGT GTT TAT Gln Ala Leu Ile Asp Tyr Ile Lys Ser Asp Phe Asp Leu Gly Val Tyr 710 715 720			2276
TGG AAA ACC CTG AAT GAG AAC GGA ATA ACA AAA GAG CGT CTT TTG AGT Trp Lys Thr Leu Asn Glu Asn Gly Ile Thr Lys Glu Arg Leu Leu Ser 725 730 735 740			2324
TAT GAC CGT GCT ATC CAT TCT GAA CCA AAT TTT AGA GGA GAT CAA AAG Tyr Asp Arg Ala Ile His Ser Glu Pro Asn Phe Arg Gly Asp Gln Lys 745 750 755			2372
GGT GGT CTT TTG CGT GAT TTA GGT CAC TAT ATG AGA ACA TTG AAG GCA Gly Gly Leu Leu Arg Asp Leu Gly His Tyr Met Arg Thr Leu Lys Ala 760 765 770			2420
GTT CAT TCA GGT GCA GAT CTT GAG TCT GCT ATT GCA AAC TGC ATG GGC Val His Ser Gly Ala Asp Leu Glu Ser Ala Ile Ala Asn Cys Met Gly 775 780 785			2468
TAC AAA ACT GAG GGA GAA GGC TTT ATG GTT GGA GTC CAG ATA AAT CCT Tyr Lys Thr Glu Gly Glu Gly Phe Met Val Gly Val Gln Ile Asn Pro 790 795 800			2516
GTA TCA GGC TTG CCA TCT GGC TTT CAG GAC CTC CTC CAT TTT GTC TTA Val Ser Gly Leu Pro Ser Gly Phe Gln Asp Leu Leu His Phe Val Leu 805 810 815 820			2564
GAC CAT GTG GAA GAT AAA AAT GTG GAA ACT CTT CTT GAG AGA TTG CTA Asp His Val Glu Asp Lys Asn Val Glu Thr Leu Leu Glu Arg Leu Leu 825 830 835			2612
GAG GCT CGT GAG GAG CTT AGG CCC TTG CTT CTC AAA CCA AAC AAC CGT Glu Ala Arg Glu Glu Leu Arg Pro Leu Leu Leu Lys Pro Asn Asn Arg 840 845 850			2660
CTA AAG GAT CTG CTG TTT TTG GAC ATA GCA CTT GAT TCT ACA GTT AGA Leu Lys Asp Leu Leu Phe Leu Asp Ile Ala Leu Asp Ser Thr Val Arg 855 860 865			2708
ACA GCA GTA GAA AGG GGA TAT GAA GAA TTG AAC AAC GCT AAT CCT GAG Thr Ala Val Glu Arg Gly Tyr Glu Glu Leu Asn Asn Ala Asn Pro Glu 870 875 880			2756
AAA ATC ATG TAC TTC ATC TCC CTC GTT CTT GAA AAT CTC GCA CTC TCT Lys Ile Met Tyr Phe Ile Ser Leu Val Leu Glu Asn Leu Ala Leu Ser 885 890 895 900			2804
GTG GAC GAT AAT GAA GAT CTT GTT TAT TGC TTG AAG GGA TGG AAT CAA Val Asp Asp Asn Glu Asp Leu Val Tyr Cys Leu Lys Gly Trp Asn Gln 905 910 915			2852
GCT CTT TCA ATG TCC AAT GGT GGG GAC AAC CAT TGG GCT TTA TTT GCA Ala Leu Ser Met Ser Asn Gly Gly Asp Asn His Trp Ala Leu Phe Ala 920 925 930			2900
AAA GCT GTG CTT GAC AGA ACC CGT CTT GCA CTT GCA AGC AAG GCA GAG Lys Ala Val Leu Asp Arg Thr Arg Leu Ala Leu Ala Ser Lys Ala Glu 935 940 945			2948
TGG TAC CAT CAC TTA TTG CAG CCA TCT GCC GAA TAT CTA GGA TCA ATA Trp Tyr His His Leu Leu Gln Pro Ser Ala Glu Tyr Leu Gly Ser Ile 950 955 960			2996

950	CTT GGG GTG GAC CAA TGG GCT TTG AAC ATA TTT ACT GAA GAA ATT ATA Leu Gly Val Asp Gln Trp Ala Leu Asn Ile Phe Thr Glu Glu Ile Ile 965 970 975 980	3044
	CGT GCT GGA TCA GCA GCT TCA TTA TCC TCT CTT CTT AAT AGA CTC GAT Arg Ala Gly Ser Ala Ala Ser Leu Ser Ser Leu Leu Asn Arg Leu Asp 985 990 995	3092
	CCC GTG CTT CGG AAA ACT GCA AAT CTA GGA AGT TGG CAG ATT ATC AGT Pro Val Leu Arg Lys Thr Ala Asn Leu Gly Ser Trp Gln Ile Ile Ser 1000 1005 1010	3140
	CCA GTT GAA GCC GTT GGA TAT GTT GTC GTT GTG GAT GAG TTG CTT TCA Pro Val Glu Ala Val Gly Tyr Val Val Val Val Asp Glu Leu Leu Ser 1015 1020 1025	3188
	GTT CAG AAT GAA ATC TAC GAG AAG CCC ACG ATC TTA GTA GCA AAA TCT Val Gln Asn Glu Ile Tyr Glu Lys Pro Thr Ile Leu Val Ala Lys Ser 1030 1035 1040	3236
	GTT AAA GGA GAG GAG GAA ATT CCT GAT GGT GCT GTT GCC CTG ATA ACA Val Lys Gly Glu Glu Glu Ile Pro Asp Gly Ala Val Ala Leu Ile Thr 1045 1050 1055 1060	3284
	CCA GAC ATG CCA GAT GTT CTT TCA CAT GTT TCT GTT CGA GCT AGA AAT Pro Asp Met Pro Asp Val Leu Ser His Val Ser Val Arg Ala Asn 1065 1070 1075	3332
	GGG AAG GTT TGC TTT GCT ACA TGC TTT GAT CCC AAT ATA TTG GCT GAC Gly Lys Val Cys Phe Ala Thr Cys Phe Asp Pro Asn Ile Leu Ala Asp 1080 1085 1090	3380
	CTC CAA GCA AAG GAA GGA AGG ATT TTG CTC TTA AAG CCT ACA CCT TCA Leu Gln Ala Lys Glu Gly Arg Ile Leu Leu Leu Lys Pro Thr Pro Ser 1095 1100 1105	3428
	GAC ATA ATC TAT AGT GAG GTG AAT GAG ATT GAG CTC CAA AGT TCA AGT Asp Ile Ile Tyr Ser Glu Val Asn Glu Ile Glu Leu Gln Ser Ser Ser 1110 1115 1120	3476
	AAC TTG GTA GAA GCT GAA ACT TCA GCA ACA CTT AGA TTG GTG AAA AAG Asn Leu Val Glu Ala Glu Thr Ser Ala Thr Leu Arg Leu Val Lys Lys 1125 1130 1135 1140	3524
	CAA TTT GGT GGT TGT TAC GCA ATA TCA GCA GAT GAA TTC ACA AGT GAA Gln Phe Gly Gly Cys Tyr Ala Ile Ser Ala Asp Glu Phe Thr Ser Glu 1145 1150 1155	3572
	ATG GTT GGA GCT AAA TCA CGT AAT ATT GCA TAT CTG AAA GGA AAA GTG Met Val Gly Ala Lys Ser Arg Asn Ile Ala Tyr Leu Lys Gly Lys Val 1160 1165 1170	3620
	CCT TCC TCG GTG GGA ATT CCT ACG TCA GTA GCT CTT CCA TTT GGA GTC Pro Ser Ser Val Gly Ile Pro Thr Ser Val Ala Leu Pro Phe Gly Val 1175 1180 1185	3668
	TTT GAG AAA GTA CTT TCA GAC GAC ATA AAT CAG GGA GTG GCA AAA GAG Phe Glu Lys Val Leu Ser Asp Asp Ile Asn Gln Gly Val Ala Lys Glu 1190 1195 1200	3716
	TTG CAA ATT CTG ATG AAA AAA CTA TCT GAA GGA GAC TTC AGC GCT CTT	3764

Leu Gln Ile Leu Met Lys Lys Leu Ser Glu Gly Asp Phe Ser Ala Leu 1205 1210 1215 1220	
GGT GAA ATT CGC ACA ACG GTT TTA GAT CTT TCA GCA CCA GCT CAA TTG Gly Glu Ile Arg Thr Thr Val Leu Asp Leu Ser Ala Pro Ala Gln Leu 1225 1230 1235	3812
GTC AAA GAG CTG AAG GAG AAG ATG CAG GGT TCT GGC ATG CCT TGG CCT Val Lys Glu Leu Lys Glu Lys Met Gln Gly Ser Gly Met Pro Trp Pro 1240 1245 1250	3860
GGT GAT GAA GGT CCA AAG CGG TGG GAA CAA GCA TGG ATG GCC ATA AAA Gly Asp Glu Gly Pro Lys Arg Trp Glu Gln Ala Trp Met Ala Ile Lys 1255 1260 1265	3908
AAG GTG TGG GCT TCA AAA TGG AAT GAG AGA GCA TAC TTC AGC ACA AGG Lys Val Trp Ala Ser Lys Trp Asn Glu Arg Ala Tyr Phe Ser Thr Arg 1270 1275 1280	3956
AAG GTG AAA CTG GAT CAT GAC TAT CTG TGC ATG GCT GTC CTT GTT CAA Lys Val Lys Leu Asp His Asp Tyr Leu Cys Met Ala Val Leu Val Gln 1285 1290 1295 1300	4004
GAA ATA ATA AAT GCT GAT TAT GCA TTT GTC ATT CAC ACA ACC AAC CCA Glu Ile Ile Asn Ala Asp Tyr Ala Phe Val Ile His Thr Thr Asn Pro 1305 1310 1315	4052
TCT TCC GGA GAC GAC TCA GAA ATA TAT GCC GAG GTG GTC AGG GGC CTT Ser Ser Gly Asp Asp Ser Glu Ile Tyr Ala Glu Val Val Arg Gly Leu 1320 1325 1330	4100
GGG GAA ACA CTT GTT GGA GCT TAT CCA GGA CGT GCT TTG AGT TTT ATC Gly Glu Thr Leu Val Gly Ala Tyr Pro Glu Arg Ala Leu Ser Phe Ile 1335 1340 1345	4148
TGC AAG AAA AAG GAT CTC AAC TCT CCT CAA GTG TTA GGT TAC CCA AGC Cys Lys Lys Lys Asp Leu Asn Ser Pro Gln Val Leu Gly Tyr Pro Ser 1350 1355 1360	4196
AAA CCG ATC GGC CTT TTC ATA AAA AGA TCT ATC ATC TTC CGA TCT GAT Lys Pro Ile Gly Leu Phe Ile Lys Arg Ser Ile Ile Phe Arg Ser Asp 1365 1370 1375 1380	4244
TCC AAT GGG GAA GAT TTG GAA GGT TAT GCC GGT GCT GGC CTC TAC GAC Ser Asn Gly Glu Asp Leu Glu Gly Tyr Ala Gly Ala Gly Leu Tyr Asp 1385 1390 1395	4292
AGT GTA CCA ATG GAT GAG GAG GAA AAA GTT GTA ATT GAT TAC TCT TCC Ser Val Pro Met Asp Glu Glu Glu Lys Val Val Ile Asp Tyr Ser Ser 1400 1405 1410	4340
GAC CCA TTG ATA ACT GAT GGT AAC TTC CGC CAG ACA ATC CTG TCC AAC Asp Pro Leu Ile Thr Asp Gly Asn Phe Arg Gln Thr Ile Leu Ser Asn 1415 1420 1425	4388
ATT GCT CGT GCT GGA CAT GCT ATC GAG GAG CTA TAT GGC TCT CCT CAA Ile Ala Arg Ala Gly His Ala Ile Glu Glu Leu Tyr Gly Ser Pro Gln 1430 1435 1440	4436
GAC ATT GAG GGT GTA GTG AGG GAT GGA AAG ATT TAT GTC GTT CAG ACA Asp Ile Glu Gly Val Val Arg Asp Gly Lys Ile Tyr Val Val Gln Thr 1445 1450 1455 1460	4484



AGA CCA CAG ATG T GATTATATTC TCGTTGTATG TTGTTTCAGAG AAGACCACAG 4537  
Arg Pro Gln Met

ATGTGATCAT ATTCTCATTG TATCAGATCT GTGACCACTT ACCTGATACC TCCCATGAAG 4597  
TTACCTGTAT GATTATACGT GATCCAAAGC CATCACATCA TGTTACCTT CAGCTATTGG 4657  
AGGAGAAGTG AGAAGTAGGA ATTGCAATAT GAGGAATAAT AAGAAAAACT TTGTAAAAGC 4717  
TAAATTAGCT GGGTATGATA TAGGGAGAAA TGTGTAACA TTGTACTATA TATAGTATAT 4777  
ACACACGCAT TATGTATTGC ATTATGCACT GAATAATATC GCAGCATCAA AGAAGAAATC 4837  
CTTTGGGTGG TTTCAAAAA 4856

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1464 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Ser	Asn	Ser	Leu	Gly	Asn	Asn	Leu	Leu	Tyr	Gln	Gly	Phe	Leu	Thr	1	5	10	15
Ser	Thr	Val	Leu	Glu	His	Lys	Ser	Arg	Ile	Ser	Pro	Pro	Cys	Val	Gly	20	25	30	
Gly	Asn	Ser	Leu	Phe	Gln	Gln	Gln	Val	Ile	Ser	Lys	Ser	Pro	Leu	Ser	35	40	45	
Thr	Glu	Phe	Arg	Gly	Asn	Arg	Leu	Lys	Val	Gln	Lys	Lys	Lys	Ile	Pro	50	55	60	
Met	Glu	Lys	Lys	Arg	Ala	Phe	Ser	Ser	Ser	Pro	His	Ala	Val	Leu	Thr	65	70	75	80
Thr	Asp	Thr	Ser	Ser	Glu	Leu	Ala	Glu	Lys	Phe	Ser	Leu	Gly	Gly	Asn	85	90	95	
Ile	Glu	Leu	Gln	Val	Asp	Val	Arg	Pro	Pro	Thr	Ser	Gly	Asp	Val	Ser	100	105	110	
Phe	Val	Asp	Phe	Gln	Val	Thr	Asn	Gly	Ser	Asp	Lys	Leu	Phe	Leu	His	115	120	125	
Trp	Gly	Ala	Val	Lys	Phe	Gly	Lys	Glu	Thr	Trp	Ser	Leu	Pro	Asn	Asp	130	135	140	
Arg	Pro	Asp	Gly	Thr	Lys	Val	Tyr	Lys	Asn	Lys	Ala	Leu	Arg	Thr	Pro	145	150	155	160
Phe	Val	Lys	Ser	Gly	Ser	Asn	Ser	Ile	Leu	Arg	Leu	Glu	Ile	Arg	Asp	165	170	175	
Thr	Ala	Ile	Glu	Ala	Ile	Glu	Phe	Leu	Ile	Tyr	Asp	Glu	Ala	His	Asp	180	185	190	

Lys Trp Ile Lys Asn Asn Gly Gly Asn Phe Arg Val Lys Leu Ser Arg  
 195 200 205  
 Lys Glu Ile Arg Gly Pro Asp Val Ser Val Pro Glu Glu Leu Val Gln  
 210 215 220  
 Ile Gln Ser Tyr Leu Arg Trp Glu Arg Lys Gly Lys Gln Asn Tyr Pro  
 225 230 235 240  
 Pro Glu Lys Glu Lys Glu Glu Tyr Glu Ala Ala Arg Thr Val Leu Gln  
 245 250 255  
 Glu Glu Ile Ala Arg Gly Ala Ser Ile Gln Asp Ile Arg Ala Arg Leu  
 260 265 270  
 Thr Lys Thr Asn Asp Lys Ser Gln Ser Lys Glu Glu Pro Leu His Val  
 275 280 285  
 Thr Lys Ser Asp Ile Pro Asp Asp Leu Ala Gln Ala Gln Ala Tyr Ile  
 290 295 300  
 Arg Trp Glu Lys Ala Gly Lys Pro Asn Tyr Pro Pro Glu Lys Gln Ile  
 305 310 315 320  
 Glu Glu Leu Glu Glu Ala Arg Arg Glu Leu Gln Leu Glu Leu Glu Lys  
 325 330 335  
 Gly Ile Thr Leu Asp Glu Leu Arg Lys Thr Ile Thr Lys Gly Glu Ile  
 340 345 350  
 Lys Thr Lys Val Glu Lys His Leu Lys Arg Ser Ser Phe Ala Val Glu  
 355 360 365  
 Arg Ile Gln Arg Lys Lys Arg Asp Phe Gly His Leu Ile Asn Lys Tyr  
 370 375 380  
 Thr Ser Ser Pro Ala Val Gln Val Gln Lys Val Leu Glu Glu Pro Pro  
 385 390 395 400  
 Ala Leu Ser Lys Ile Lys Leu Tyr Ala Lys Glu Lys Glu Glu Gln Ile  
 405 410 415  
 Asp Asp Pro Ile Leu Asn Lys Lys Ile Phe Lys Val Asp Asp Gly Glu  
 420 425 430  
 Leu Leu Val Leu Val Ala Lys Ser Ser Gly Lys Thr Lys Val His Leu  
 435 440 445  
 Ala Thr Asp Leu Asn Gln Pro Ile Thr Leu His Trp Ala Leu Ser Lys  
 450 455 460  
 Ser Pro Gly Glu Trp Met Val Pro Pro Ser Ser Ile Leu Pro Pro Gly  
 465 470 475 480  
 Ser Ile Ile Leu Asp Lys Ala Ala Glu Thr Pro Phe Ser Ala Ser Ser  
 485 490 495  
 Ser Asp Gly Leu Thr Ser Lys Val Gln Ser Leu Asp Ile Val Ile Glu  
 500 505 510  
 Asp Gly Asn Phe Val Gly Met Pro Phe Val Leu Leu Ser Gly Glu Lys  
 515 520 525

Trp Ile Lys Asn Gln Gly Ser Asp Phe Tyr Val Gly Phe Ser Ala Ala  
 530 535 540  
 Ser Lys Leu Ala Leu Lys Ala Ala Gly Asp Gly Ser Gly Thr Ala Lys  
 545 550 555 560  
 Ser Leu Leu Asp Lys Ile Ala Asp Met Glu Ser Glu Ala Gln Lys Ser  
 565 570 575  
 Phe Met His Arg Phe Asn Ile Ala Ala Asp Leu Ile Glu Asp Ala Thr  
 580 585 590  
 Ser Ala Gly Glu Leu Gly Phe Ala Gly Ile Leu Val Trp Met Arg Phe  
 595 600 605  
 Met Ala Thr Arg Gln Leu Ile Trp Asn Lys Asn Tyr Asn Val Lys Pro  
 610 615 620  
 Arg Glu Ile Ser Lys Ala Gln Asp Arg Leu Thr Asp Leu Leu Gln Asn  
 625 630 635 640  
 Ala Phe Thr Ser His Pro Gln Tyr Arg Glu Ile Leu Arg Met Ile Met  
 645 650 655  
 Ser Thr Val Gly Arg Gly Gly Glu Gly Asp Val Gly Gln Arg Ile Arg  
 660 665 670  
 Asp Glu Ile Leu Val Ile Gln Arg Asn Asn Asp Cys Lys Gly Gly Met  
 675 680 685  
 Met Gln Glu Trp His Gln Lys Leu His Asn Asn Thr Ser Pro Asp Asp  
 690 695 700  
 Val Val Ile Cys Gln Ala Leu Ile Asp Tyr Ile Lys Ser Asp Phe Asp  
 705 710 715 720  
 Leu Gly Val Tyr Trp Lys Thr Leu Asn Glu Asn Gly Ile Thr Lys Glu  
 725 730 735  
 Arg Leu Leu Ser Tyr Asp Arg Ala Ile His Ser Glu Pro Asn Phe Arg  
 740 745 750  
 Gly Asp Gln Lys Gly Gly Leu Leu Arg Asp Leu Gly His Tyr Met Arg  
 755 760 765  
 Thr Leu Lys Ala Val His Ser Gly Ala Asp Leu Glu Ser Ala Ile Ala  
 770 775 780  
 Asn Cys Met Gly Tyr Lys Thr Glu Gly Glu Gly Phe Met Val Gly Val  
 785 790 795 800  
 Gln Ile Asn Pro Val Ser Gly Leu Pro Ser Gly Phe Gln Asp Leu Leu  
 805 810 815  
 His Phe Val Leu Asp His Val Glu Asp Lys Asn Val Glu Thr Leu Leu  
 820 825 830  
 Glu Arg Leu Leu Glu Ala Arg Glu Glu Leu Arg Pro Leu Leu Lys  
 835 840 845  
 Pro Asn Asn Arg Leu Lys Asp Leu Leu Phe Leu Asp Ile Ala Leu Asp  
 850 855 860

Ser Thr Val Arg Thr Ala Val Glu Arg Gly Tyr Glu Glu Leu Asn Asn  
 865 870 875 880  
 Ala Asn Pro Glu Lys Ile Met Tyr Phe Ile Ser Leu Val Leu Glu Asn  
 885 890 895  
 Leu Ala Leu Ser Val Asp Asp Asn Glu Asp Leu Val Tyr Cys Leu Lys  
 900 905 910  
 Gly Trp Asn Gln Ala Leu Ser Met Ser Asn Gly Gly Asp Asn His Trp  
 915 920 925  
 Ala Leu Phe Ala Lys Ala Val Leu Asp Arg Thr Arg Leu Ala Leu Ala  
 930 935 940  
 Ser Lys Ala Glu Trp Tyr His His Leu Leu Gln Pro Ser Ala Glu Tyr  
 945 950 955 960  
 Leu Gly Ser Ile Leu Gly Val Asp Gln Trp Ala Leu Asn Ile Phe Thr  
 965 970 975  
 Glu Glu Ile Ile Arg Ala Gly Ser Ala Ala Ser Leu Ser Ser Leu Leu  
 980 985 990  
 Asn Arg Leu Asp Pro Val Leu Arg Lys Thr Ala Asn Leu Gly Ser Trp  
 995 1000 1005  
 Gln Ile Ile Ser Pro Val Glu Ala Val Gly Tyr Val Val Val Asp  
 1010 1015 1020  
 Glu Leu Leu Ser Val Gln Asn Glu Ile Tyr Glu Lys Pro Thr Ile Leu  
 1025 1030 1035 1040  
 Val Ala Lys Ser Val Lys Gly Glu Glu Glu Ile Pro Asp Gly Ala Val  
 1045 1050 1055  
 Ala Leu Ile Thr Pro Asp Met Pro Asp Val Leu Ser His Val Ser Val  
 1060 1065 1070  
 Arg Ala Arg Asn Gly Lys Val Cys Phe Ala Thr Cys Phe Asp Pro Asn  
 1075 1080 1085  
 Ile Leu Ala Asp Lys Gln Ala Lys Glu Gly Arg Ile Leu Leu Leu Lys  
 1090 1095 1100  
 Pro Thr Pro Ser Asp Ile Ile Tyr Ser Glu Val Asn Glu Ile Glu Leu  
 1105 1110 1115 1120  
 Gln Ser Ser Ser Asn Leu Val Glu Ala Glu Thr Ser Ala Thr Leu Arg  
 1125 1130 1135  
 Leu Val Lys Lys Gln Phe Gly Gly Cys Tyr Ala Ile Ser Ala Asp Glu  
 1140 1145 1150  
 Phe Thr Ser Glu Met Val Gly Ala Lys Ser Arg Asn Ile Ala Tyr Leu  
 1155 1160 1165  
 Lys Gly Lys Val Pro Ser Ser Val Gly Ile Pro Thr Ser Val Ala Leu  
 1170 1175 1180  
 Pro Phe Gly Val Phe Glu Lys Val Leu Ser Asp Asp Ile Asn Gln Gly  
 1185 1190 1195 1200

Val Ala Lys Glu Leu Gln Ile Leu Met Lys Lys Leu Ser Glu Gly Asp  
 1205 1210 1215  
 Phe Ser Ala Leu Gly Glu Ile Arg Thr Thr Val Leu Asp Leu Ser Ala  
 1220 1225 1230  
 Pro Ala Gln Leu Val Lys Glu Leu Lys Glu Lys Met Gln Gly Ser Gly  
 1235 1240 1245  
 Met Pro Trp Pro Gly Asp Glu Gly Pro Lys Arg Trp Glu Gln Ala Trp  
 1250 1255 1260  
 Met Ala Ile Lys Lys Val Trp Ala Ser Lys Trp Asn Glu Arg Ala Tyr  
 1265 1270 1275 1280  
 Phe Ser Thr Arg Lys Val Lys Leu Asp His Asp Tyr Leu Cys Met Ala  
 1285 1290 1295  
 Val Leu Val Gln Glu Ile Ile Asn Ala Asp Tyr Ala Phe Val Ile His  
 1300 1305 1310  
 Thr Thr Asn Pro Ser Ser Gly Asp Asp Ser Glu Ile Tyr Ala Glu Val  
 1315 1320 1325  
 Val Arg Gly Leu Gly Glu Thr Leu Val Gly Ala Tyr Pro Gly Arg Ala  
 1330 1335 1340  
 Leu Ser Phe Ile Cys Lys Lys Asp Leu Asn Ser Pro Gln Val Leu  
 1345 1350 1355 1360  
 Gly Tyr Pro Ser Lys Pro Ile Gly Leu Phe Ile Lys Arg Ser Ile Ile  
 1365 1370 1375  
 Phe Arg Ser Asp Ser Asn Gly Glu Asp Leu Glu Gly Tyr Ala Gly Ala  
 1380 1385 1390  
 Gly Leu Tyr Asp Ser Val Pro Met Asp Glu Glu Glu Lys Val Val Ile  
 1395 1400 1405  
 Asp Tyr Ser Ser Asp Pro Leu Ile Thr Asp Gly Asn Phe Arg Gln Thr  
 1410 1415 1420  
 Ile Leu Ser Asn Ile Ala Arg Ala Gly His Ala Ile Glu Glu Leu Tyr  
 1425 1430 1435 1440  
 Gly Ser Pro Gln Asp Ile Glu Gly Val Val Arg Asp Gly Lys Ile Tyr  
 1445 1450 1455  
 Val Val Gln Thr Arg Pro Gln Met  
 1460

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1918 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Solanum tuberosum

(B) STRAIN: C.V. Desiree

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..1555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCA GAG TGG TAC CAT CAC TTA TTG CAG CCA TCT GCC GAA TAT CTA GGA	48
Ala Glu Trp Tyr His His Leu Leu Gln Pro Ser Ala Glu Tyr Leu Gly	
1 5 10 15	
TCA ATA CTT GGG GTG GAC CAA TGG GCT TTG AAC ATA TTT ACT GAA GAA	96
Ser Ile Leu Gly Val Asp Gln Trp Ala Leu Asn Ile Phe Thr Glu Glu	
20 25 30	
ATT ATA CGT GCT GGA TCA GCA GCT TCA TTA TCC TCT CTT CTT AAT AGA	144
Ile Ile Arg Ala Gly Ser Ala Ala Ser Leu Ser Ser Leu Leu Asn Arg	
35 40 45	
CTC GAT CCC GTG CTT CGG AAA ACT GCA AAT CTA GGA AGT TGG CAG ATT	192
Leu Asp Pro Val Leu Arg Lys Thr Ala Asn Leu Gly Ser Trp Gln Ile	
50 55 60	
ATC AGT CCA GTT GAA GCC GTT GGA TAT GTT GTC GTT GTG GAT GAG TTG	240
Ile Ser Pro Val Glu Ala Val Gly Tyr Val Val Val Val Asp Glu Leu	
65 70 75 80	
CTT TCA GTT CAG AAT GAA ATC TAC GAG AAG CCC ACG ATC TTA GTA GCA	288
Leu Ser Val Gln Asn Glu Ile Tyr Glu Lys Pro Thr Ile Leu Val Ala	
85 90 95	
AAA TCT GTT AAA GGA GAG GAG GAA ATT CCT GAT GGT GCT GTT GCC CTG	336
Lys Ser Val Lys Gly Glu Glu Glu Ile Pro Asp Gly Ala Val Ala Leu	
100 105 110	
ATA ACA CCA GAC ATG CCA GAT GTT CTT TCA CAT GTT TCT CGA GCT	384
Ile Thr Pro Asp Met Pro Asp Val Leu Ser His Val Ser Val Arg Ala	
115 120 125	
AGA ART GGG AAG GTT TGC TTT GCT ACA TGC TTT GAT CCC AAT ATA TTG	432
Arg Asn Gly Lys Val Cys Phe Ala Thr Cys Phe Asp Pro Asn Ile Leu	
130 135 140	
GCT GAC CTC CAA GCA AAG GAA GGA AGG ATT TTG CTC TTA AAG CCT ACA	480
Ala Asp Leu Gln Ala Lys Glu Gly Arg Ile Leu Leu Leu Lys Pro Thr	
145 150 155 160	
CCT TCA GAC ATA ATC TAT AGT GAG GTG AAT GAG ATT GAG CTC CAA AGT	528
Pro Ser Asp Ile Ile Tyr Ser Glu Val Asn Glu Ile Glu Leu Gln Ser	
165 170 175	
TCA AGT AAC TTG GTA GAA GCT GAA ACT TCA GCA ACA CTT AGA TTG GTG	576
Ser Ser Asn Leu Val Glu Ala Glu Thr Ser Ala Thr Leu Arg Leu Val	
180 185 190	
AAA AAG CAA TTT GGT GGT TGT TAC GCA ATA TCA GCA GAT GAA TTC ACA	624
Lys Lys Gln Phe Gly Gly Cys Tyr Ala Ile Ser Ala Asp Glu Phe Thr	
195 200 205	
AGT GAA ATG GTT GGA GCT AAA TCA CGT AAT ATT GCA TAT CTG AAA GGA	672
Ser Glu Met Val Gly Ala Lys Ser Arg Asn Ile Ala Tyr Leu Lys Gly	
210 215 220	

AAA GTG CCT TCC TCG GTG GGA ATT CCT ACG TCA GTA GCT CTT CCA TTT Lys Val Pro Ser Ser Val Gly Ile Pro Thr Ser Val Ala Leu Pro Phe 225 230 235 240	720
GGA GTC TTT GAG AAA GTA CTT TCA GAC GAC ATA AAT CAG GGA GTG GCA Gly Val Phe Glu Lys Val Leu Ser Asp Asp Ile Asn Gln Gly Val Ala 245 250 255	768
AAA GAG TTG CAA ATT CTG ACA AAA AAA CTA TCT GAA GGA GAC TTT AGC Lys Glu Leu Gln Ile Leu Thr Lys Lys Leu Ser Glu Gly Asp Phe Ser 260 265 270	816
GCT CTT GGT GAA ATT CGC ACA ACG GTT TTA GAT CTT TCG ACA CCA GCT Ala Leu Gly Glu Ile Arg Thr Thr Val Leu Asp Leu Ser Thr Pro Ala 275 280 285	864
CAA TTG GTC AAA GAG CTG AAG GAG AAG ATG CAG GGT TCT GGC ATG CCT Gln Leu Val Lys Glu Leu Lys Glu Lys Met Gln Ser Gly Met Pro 290 295 300	912
TGG CCT GGT GAT GAA GGT CCA AAG CGG TGG GAA CAA GCA TGG ATG GCC Trp Pro Gly Asp Glu Gly Pro Lys Arg Trp Glu Gln Ala Trp Met Ala 305 310 315 320	960
ATA AAA AAG GTG TGG GCT TCA AAA TGG AAT GAG AGA GCA TAC TTC AGC Ile Lys Lys Val Trp Ala Ser Lys Trp Asn Glu Arg Ala Tyr Phe Ser 325 330 335	1008
ACA AGG AAG GTG AAA CTG GAT CAT GAC TAT CTG TGC ATG GCT GTC CTT Thr Arg Lys Val Lys Leu Asp His Asp Tyr Leu Cys Met Ala Val Leu 340 345 350	1056
GTT CAA GAA ATA ATA AAT GCT GAT TAT GCA TTT GTC ATT CAC ACA ACC Val Gln Glu Ile Ile Asn Ala Asp Tyr Ala Phe Val Ile His Thr Thr 355 360 365	1104
AAC CCA TCT TCC GGA GAC GAC TCA GAA ATA TAT GCC GAG GTG GTC AGG Asn Pro Ser Ser Gly Asp Asp Ser Glu Ile Tyr Ala Glu Val Val Arg 370 375 380	1152
GGC CTT GGG GAA ACA CTT GTT GGA GCT TAT CCA GGA CGT GCT TTG AGT Gly Leu Gly Glu Thr Leu Val Gly Ala Tyr Pro Gly Arg Ala Leu Ser 385 390 395 400	1200
TTT ATC TGC AAG AAA AAG GAT CTC AAC TCT CCT CAA GTG TTA GGT TAC Phe Ile Cys Lys Lys Lys Asp Leu Asn Ser Pro Gln Val Leu Gly Tyr 405 410 415	1248
CCA AGC AAA CCG ATC GGC CTT TTC ATA AAA AGA TCT ATC ATC TTC CGA Pro Ser Lys Pro Ile Gly Leu Phe Ile Lys Arg Ser Ile Ile Phe Arg 420 425 430	1296
TCT GAT TCC AAT GGG GAA GAT TTG GAA GGT TAT GCC GGT GCT GGC CTC Ser Asp Ser Asn Gly Glu Asp Leu Glu Gly Tyr Ala Gly Ala Gly Leu 435 440 445	1344
TAC GAC AGT GTA CCA ATG GAT GAG GAG GAA AAA GTT GTA ATT GAT TAC Tyr Asp Ser Val Pro Met Asp Glu Glu Glu Lys Val Val Ile Asp Tyr 450 455 460	1392
TCT TCC GAC CCA TTG ATA ACT GAT GGT AAC TTC CGC CAG ACA ATC CTG Ser Ser Asp Pro Leu Ile Thr Asp Gly Asn Phe Arg Gln Thr Ile Leu 465 470 475 480	1440

TCC AAC ATT GCT CGT GCT GGA CAT GCT ATC GAG GAG CTA TAT GGC TCT	1488
Ser Asn Ile Ala Arg Ala Gly His Ala Ile Glu Glu Leu Tyr Gly Ser	
485 490 495	
CCT CAA GAC ATT GAG GGT GTA GTG AGG GAT GGA AAG ATT TAT GTC GTT	1536
Pro Gln Asp Ile Glu Gly Val Val Arg Asp Gly Lys Ile Tyr Val Val	
500 505 510	
CAG ACA AGA CCA CAG ATG T GATTATATTC TCGTTGTATG TTGTTGAGAG	1585
Gln Thr Arg Pro Gln Met	
515	
AAGACCACAG ATGTGATCAT ATTCTCATTG TATCAGATCT GTGACCACTT ACCTGATACC	1645
TCCCATGAAG TTACCTGTAT GATTATACGT GATCCAAAGC CATCACATCA TGTTCACCTT	1705
CAGCTATTGG AGGAGAAGTG AGAAGTAGGA ATTGCAATAT GAGGAATAAT AAGAAAAACT	1765
TTGTAAGAAC TAAATTAGCT GGGTATGATA TAGGGAGAAA TGTGTAACAA TTGTACTATA	1825
TATAGTATAT ACACACGCAT TATGTATTGC ATTATGCACT GAATAATATC GCAGCATCAA	1885
AGAAGAAATC CTTTGGGTGG TTTCAAAAAA AAA	1918

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 518 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Ala Glu Trp Tyr His His Leu Leu Gln Pro Ser Ala Glu Tyr Leu Gly	
1 5 10 15	
Ser Ile Leu Gly Val Asp Gln Trp Ala Leu Asn Ile Phe Thr Glu Glu	
20 25 30	
Ile Ile Arg Ala Gly Ser Ala Ala Ser Leu Ser Ser Leu Leu Asn Arg	
35 40 45	
Leu Asp Pro Val Leu Arg Lys Thr Ala Asn Leu Gly Ser Trp Gln Ile	
50 55 60	
Ile Ser Pro Val Glu Ala Val Gly Tyr Val Val Val Val Asp Glu Leu	
65 70 75 80	
Leu Ser Val Gln Asn Glu Ile Tyr Glu Lys Pro Thr Ile Leu Val Ala	
85 90 95	
Lys Ser Val Lys Gly Glu Glu Glu Ile Pro Asp Gly Ala Val Ala Leu	
100 105 110	
Ile Thr Pro Asp Met Pro Asp Val Leu Ser His Val Ser Val Arg Ala	
115 120 125	
Arg Asn Gly Lys Val Cys Phe Ala Thr Cys Phe Asp Pro Asn Ile Leu	
130 135 140	
Ala Asp Leu Gln Ala Lys Glu Gly Arg Ile Leu Leu Leu Lys Pro Thr	
145 150 155 160	



Pro Ser Asp Ile Ile Tyr Ser Glu Val Asn Glu Ile Glu Leu Gln Ser  
 165 170 175  
 Ser Ser Asn Leu Val Glu Ala Glu Thr Ser Ala Thr Leu Arg Leu Val  
 180 185 190  
 Lys Lys Gln Phe Gly Gly Cys Tyr Ala Ile Ser Ala Asp Glu Phe Thr  
 195 200 205  
 Ser Glu Met Val Gly Ala Lys Ser Arg Asn Ile Ala Tyr Leu Lys Gly  
 210 215 220  
 Lys Val Pro Ser Ser Val Gly Ile Pro Thr Ser Val Ala Leu Pro Phe  
 225 230 235  
 Gly Val Phe Glu Lys Val Leu Ser Asp Asp Ile Asn Gln Gly Val Ala  
 245 250 255  
 Lys Glu Leu Gln Ile Leu Thr Lys Lys Leu Ser Glu Gly Asp Phe Ser  
 260 265 270  
 Ala Leu Gly Glu Ile Arg Thr Thr Val Leu Asp Leu Ser Thr Pro Ala  
 275 280 285  
 Gln Leu Val Lys Glu Leu Lys Glu Lys Met Gln Gly Ser Gly Met Pro  
 290 295 300  
 Trp Pro Gly Asp Glu Gly Pro Lys Arg Trp Glu Gln Ala Trp Met Ala  
 305 310 315 320  
 Ile Lys Lys Val Trp Ala Ser Lys Trp Asn Glu Arg Ala Tyr Phe Ser  
 325 330 335  
 Thr Arg Lys Val Lys Leu Asp His Asp Tyr Leu Cys Met Ala Val Leu  
 340 345 350  
 Val Gln Glu Ile Ile Asn Ala Asp Tyr Ala Phe Val Ile His Thr Thr  
 355 360 365  
 Asn Pro Ser Ser Gly Asp Asp Ser Glu Ile Tyr Ala Glu Val Val Arg  
 370 375 380  
 Gly Leu Gly Glu Thr Leu Val Gly Ala Tyr Pro Gly Arg Ala Leu Ser  
 385 390 395 400  
 Phe Ile Cys Lys Lys Lys Asp Leu Asn Ser Pro Gln Val Leu Gly Tyr  
 405 410 415  
 Pro Ser Lys Pro Ile Gly Leu Phe Ile Lys Arg Ser Ile Ile Phe Arg  
 420 425 430  
 Ser Asp Ser Asn Gly Glu Asp Leu Glu Gly Tyr Ala Gly Ala Gly Leu  
 435 440 445  
 Tyr Asp Ser Val Pro Met Asp Glu Glu Glu Lys Val Val Ile Asp Tyr  
 450 455 460  
 Ser Ser Asp Pro Leu Ile Thr Asp Gly Asn Phe Arg Gln Thr Ile Leu  
 465 470 475 480  
 Ser Asn Ile Ala Arg Ala Gly His Ala Ile Glu Glu Leu Tyr Gly Ser  
 485 490 495

Pro Gln Asp Ile Glu Gly Val Val Arg Asp Gly Lys Ile Tyr Val Val  
500 505 510

Gln Thr Arg Pro Gln Met  
515

[illegible]